

CG/872.852

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2003, 14:53:17 ; Search time 69 Seconds
without alignments!
109.213 Million cell updates/sec

Title: US-09-872-852-4
Perfect score: 250
Sequence: : GINTLQNYVVRVSGRCAYKEQIGKCTGRKCRPKK 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 62382 seqs, 16745610 residues
Total number of hits satisfying chosen parameters: 62382

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.
2: /cgn2_6/ptodata/1/pubpaa/PTX_NEX_PUB.pep.
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PTB.pep.
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PTB.pep.
6: /cgn2_6/ptodata/1/pubpaa/PTJ6_PUBCOMB.pep.
7: /cgn2_6/ptodata/1/pubpaa/US08_NEX_PUB.pep.
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PTB.pep.
13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PTB.pep.
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PTB.pep.
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	45	10	US-09-872-852-4 Sequence 4, Appl
2	250	100.0	67	9	US-09-917-340-52 Sequence 52, Appl
3	250	100.0	67	9	US-09-917-340-72 Sequence 12, Appl
4	250	100.0	67	10	US-09-872-852-2 Sequence 2, Appl
5	250	100.0	67	12	US-10-091-166B-10 Sequence 10, Appl
6	250	100.0	67	12	US-10-272-121-10 Sequence 10, Appl
7	250	100.0	67	12	US-10-409-366-10 Sequence 10, Appl
8	250	100.0	67	12	US-10-409-366-10 Sequence 10, Appl
9	240	96.0	65	12	US-10-091-166B-2 Sequence 2, Appl
10	240	96.0	65	12	US-10-272-121-2 Sequence 2, Appl
11	240	96.0	65	12	US-10-409-366-2 Sequence 2, Appl
12	240	96.0	65	12	US-10-409-366-2 Sequence 2, Appl
13	230	92.0	41	10	US-09-872-852-3 Sequence 4, Appl
14	214	85.6	45	12	US-10-091-166B-43 Sequence 43, Appl
15	214	85.6	45	12	US-10-272-121-43 Sequence 43, Appl

Sequence 43, Appl
Sequence 43, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 42, A
Sequence 42, A
Sequence 42, A
Sequence 40, App
Sequence 40, App
Sequence 40, App
Sequence 40, App
Sequence 40, App

ALIGNMENTS

RESULT :
US-09-872-852-4
Sequence 4, Application US/09/872.852
Patent No. US2002015602A1
GENERAL INFORMATION:
APPLICANT: MCCRAY JR, PAUL B.
APPLICANT: TACK, BRIAN
APPLICANT: CIA, HONG PENG
APPLICANT: SCHUTTE, BRIAN C.
TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
FILE REFERENCE: IOWA-031015
CURRENT APPLICATION NUMBER: US/09/872.852
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 601208792
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 4
LENGTH: 45
TYPE: EST
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-872-852-4

Query Match 100.0% Score 250.0 DB ID: Length 45
Best Local Similarity 100.0% Pred. No. 6.7e-24
Matches 45: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
CV : GYNTLQNYVVRVSGRCAYESGKPEQIGKCTGRKCRPKK 45
DB : GYNTLQNYVVRVSGRCAYESGKPEQIGKCTGRKCRPKK 45

RESULT 2
US-09-872-852-43

Sequence 52, Application US/0917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher C.
APPLICANT: McNulty, Jonathan P.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-29
PRIOR APPLICATION NUMBER: 60/249,632
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

Query Match 100.0%; Score 250; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 45
DB 23 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 67

RESULT 3
US-09-917-340-72
Sequence 72, Application US/0917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher C.
APPLICANT: McNulty, Jonathan P.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,632
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 72
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match 100.0%; Score 250; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 45
DB 23 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 67

RESULT 4
US-09-872-852-2
Sequence 2, Application US/09872852
Patent No. US2002011562A1
GENERAL INFORMATION:

APPLICANT: MCCRAY JR, PAUL B.
APPLICANT: TACK, BRIAN
APPLICANT: JIA, HONG PENG
APPLICANT: SCHUTTE, BRIAN C.
TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
FILE REFERENCE: JOKA-031US
CURRENT APPLICATION NUMBER: US/09/872,852
CURRENT FILING DATE: 2001-04-01
PRIOR APPLICATION NUMBER: 60/208,792
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-872-852-2

Query Match 100.0%; Score 250; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 45
DB 23 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 67

RESULT 5
US-10-391-166B-10
Sequence 10, Application US/1009166B
Publication No. US2003144551A1
GENERAL INFORMATION:
APPLICANT: Adair, David A.
APPLICANT: Holloway, James S.
APPLICANT: Baichur, Hans
APPLICANT: Betsel-Omer, Stephanie
APPLICANT: Sheppard, Paul C.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-4401
CURRENT APPLICATION NUMBER: US/10/391,166B
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/636,329
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 09/344,097
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/150,156
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 61/064,234
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 61/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-391-166B-10

Query Match 100.0%; Score 250; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 45
DB 23 GIINTLQKYYCVRGRCVAVLSCLPKKEEQIGKCKSTRGRKCCRRKK 67

RESULT 6

1 APPLICANT: TACK, BRIAN
2 APPLICANT: JIA, HONG PENG
3 APPLICANT: SCHUTTE, BRIAN C
4 TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
5 TITLE OF INVENTION: BETA-DEFENSIN ANTIMICROBIAL PEPTIDE
6 FILE REFERENCE: ICWA:031US
7 CURRENT APPLICATION NUMBER: US/09/872,852
8 PRIOR FILING DATE: 2001-06-01
9 PRIOR APPLICATION NUMBER: 60/208,782
10 PRIOR FILING DATE: 2000-05-01
11 NUMBER OF SEQ ID NOS: 24
12 SOFTWARE: Patent In Ver. 2.1
13 SEQ ID NO 3
14 LENGTH: 41
15 TYPE: PRT
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
19 OTHER INFORMATION: Peptide
20 US-09-872-852-3

Query Match 92.08; Score 210; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.9e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TLQYVCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45
DB 1 TLQYVCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 41

RESULT 14
US-10-091-166B-43
1 Sequence 43, Application US/0301166B
2 Publication No. US2003014671A1
3 GENERAL INFORMATION:
4 APPLICANT: Adler, David A.
5 APPLICANT: Holloway, James L.
6 APPLICANT: Baird, Nand
7 APPLICANT: Beigel-Orne, Stephanie
8 APPLICANT: Sheppard, Paul O.
9 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
10 FILE REFERENCE: 97-4401
11 CURRENT APPLICATION NUMBER: US/10/091,166B
12 CURRENT FILING DATE: 2002-03-05
13 PRIOR APPLICATION NUMBER: US 09/636,399
14 PRIOR FILING DATE: 2000-08-10
15 PRIOR APPLICATION NUMBER: US 09/344,097
16 PRIOR FILING DATE: 1999-06-25
17 PRIOR APPLICATION NUMBER: US 09/150,786
18 PRIOR FILING DATE: 1998-09-10
19 PRIOR APPLICATION NUMBER: US 60/064,294
20 PRIOR FILING DATE: 1997-11-30
21 PRIOR APPLICATION NUMBER: US 60/058,335
22 PRIOR FILING DATE: 1997-09-10
23 NUMBER OF SEQ ID NOS: 72
24 SOFTWARE: FastSeq for Windows Version 4.0
25 SEQ ID NO 43
26 LENGTH: 45
27 TYPE: PRT
28 ORGANISM: Artificial Sequence
29 FEATURE:
30 OTHER INFORMATION: Defensein polypeptide
31 NAME/KEY: VARIANT
32 LOCATION: (41)...(41)
33 OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
34 OTHER INFORMATION: methionine
35 US-10-091-166B-43

Query Match 85.4%; Score 214; DB 12; Length 45;
Best Local Similarity 91.1%; Pred. No. 1.9e-19;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GINTLCKVYCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45
DB 1 GINTLCKVYCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45

Search completed: October 27, 2003, 15:01:11
Job time: 1:30 secs

QY 1 GINTLCKVYCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45
DB 1 GINTLCKVYCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45

RESULT 15
US-10-072-121-43
1 Sequence 43, Application US/0207121
2 Publication No. US2003015768A1
3 GENERAL INFORMATION:
4 APPLICANT: Adler, David A.
5 APPLICANT: Holloway, James L.
6 APPLICANT: Baird, Nand
7 APPLICANT: Beigel-Orne, Stephanie
8 APPLICANT: Sheppard, Paul O.
9 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
10 FILE REFERENCE: 97-4402
11 CURRENT APPLICATION NUMBER: US/10/272,121
12 CURRENT FILING DATE: 2002-10-15
13 PRIOR APPLICATION NUMBER: US 09/636,399
14 PRIOR FILING DATE: 2000-08-10
15 PRIOR APPLICATION NUMBER: US 09/344,097
16 PRIOR FILING DATE: 1999-06-25
17 PRIOR APPLICATION NUMBER: US 09/150,786
18 PRIOR FILING DATE: 1998-09-10
19 PRIOR APPLICATION NUMBER: US 60/064,294
20 PRIOR FILING DATE: 1997-11-30
21 PRIOR APPLICATION NUMBER: US 60/058,335
22 PRIOR FILING DATE: 1997-09-10
23 NUMBER OF SEQ ID NOS: 72
24 SOFTWARE: FastSeq for Windows Version 4.0
25 SEQ ID NO 43
26 LENGTH: 45
27 TYPE: PRT
28 ORGANISM: Artificial Sequence
29 FEATURE:
30 OTHER INFORMATION: Defensein polypeptide
31 NAME/KEY: VARIANT
32 LOCATION: (41)...(41)
33 OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
34 OTHER INFORMATION: methionine
35 US-10-072-121-43

Query Match 85.4%; Score 214; DB 12; Length 45;
Best Local Similarity 91.1%; Pred. No. 1.9e-19;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GINTLCKVYCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45
DB 1 GINTLCKVYCRVGRGCAVLSCLPKKEQIGKSTGRKCKRRKK 45

Search completed: October 27, 2003, 15:01:11
Job time: 1:30 secs

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OK protein - protein search, using sw model

Run on: October 27, 2003, 14:52:02 ; Search time 16 Seconds
(without alignment)
270.474 Million cell updates/sec

Title: US-09-872-852-4
Perfect score: 250
Sequence: 1 GINTLQKYKVRGRCRAV.....KEEQIGKSTPRGKCKRRK 45
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 761*
1: PIR1*
2: PIR2*
3: PIR3*
4: PIR4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	89	35.6	42	2 F45495	beta-defensin-6 -
2	75	30.0	38	2 B47553	beta-defensin-11 -
3	73	29.2	64	2 A51128	lysozyme antimicrob
4	71	28.4	42	2 C45495	beta-defensin-3 -
5	71	28.4	64	2 A47438	airway epithelial
6	69.5	27.8	45	2 A37509	myotoxin - elastoin
7	69.5	27.8	95	1 WTRBM	macrophage antibio
8	69	27.6	40	2 G45495	beta-defensin-7 -
9	69	27.6	40	2 F45495	beta-defensin-9 -
10	68	27.2	42	2 D47753	beta-defensin-13 -
11	67.5	27.0	65	2 C35947	crotamine 3 precu
12	67.5	27.0	65	2 A35947	crotamine 1 precu
13	66.5	26.6	43	1 CX85CH	toxic peptide C -
14	65.5	26.2	42	1 CX85MT	crotamine 4 tropic
15	65.5	26.2	51	2 C35947	crotamine 4 precu
16	65.5	26.2	95	1 WTRBM2	defensin C3-4 prec
17	63.5	25.4	65	2 JC3324	tyrotoxin a precus
18	62.5	25.0	42	1 MX8SMV	myotoxin a 6 - fra
19	61	24.4	524	2 S18519	disintegrin-like 7
20	61	24.4	670	2 I45967	disintegrin-like 7
21	60.5	24.2	40	2 C15560	myotoxin a 5 - fra
22	60	24.0	32	2 E50076	defensin alpha 5 -
23	60	24.0	32	2 G50076	defensin alpha-7 -
24	60	24.0	33	2 D50076	defensin alpha-4 -
25	60	24.0	33	2 E50076	defensin alpha-6
26	59	23.6	40	2 E45495	beta-defensin-5
27	59	23.6	850	2 C05981	hypothetical prote
28	58.5	23.4	43	2 A25095	myotoxin 1 - midge
29	58.5	23.4	45	2 S15909	tyrotoxin - western

Query Match 35.64; Score 69; DB 2; Length 42;
Best local similarity 48.94; Pred. No. 3,0042;
Matches 16; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QV 11 (FVVRGKQAVLSCDFEEDQIGKSTPRGKCKRR 43
DC 9 (ATVVGQCVDFPCFPTACDCTFGRPYKCKRR 41
RESULT 2
B47753
beta-defensin-11 - bovine
N:Alternate names: peptide BMB-11
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16 Dec 1994
C:Accession: B47753
R:Seastedt, N.E.; Tang, Y.Q.; Norris, W.D.; McGuire, P.A.; Novotny, M.J.; Smith, W.J.
J. Biol. Chem. 268, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defe
A:Reference number: A45495; MIMD:91203264; PMID:8454635
A:Accession: F45495
A:Molecule type: protein
A:Residues: 1-42 «SGL»
A:Note: sequence modified after extraction from NCBI backbone
C:Keywords: antibacterial; disulfide bond; pyroglutamic acid
F:1-38/Product: beta-defensin-6 #status experimental «VAL»
F:1-Modified site: pyroglutamic acid (Gln) #status experimental
F:19-38,15-31,21-39/Disulfide bonds: #status predicted

ALIGNMENTS

high sulfur protei
probable finger pr
corticostatic pep
protamine - mouse
protamine 1 - rat
myotoxin 11 - midg
hypothetical prote
beta-defensin-1 -
genome polyprotein
Krat-2 protein - Ca
defensin alpha-5 p
epidermal growth f
epidermal growth f
epidermal growth f
epidermal growth f
galinacin - chick

Query Match 36.84; Score 70; DB 2; Length 42;
Best local similarity 46.94; Pred. No. 3,02;
Matches 16; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 11 CRVRGGRCVAVLSCLPKKEQIGKCSRGRKCKCR 42
| | | | | | | | | | | | | | | | | | | | |
DB 5 CERNGGVCIPRCGPGPRQIGTCFGRFVKCCR 36
| | | | | | | | | | | | | | | | | | | | |
RESULT 3
A56128
Lingual antimicrobial peptide precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Nov-1999
C:Accession: A56128; B56128
R:Schonwetter, B.S.; Stolzenberg, E.L.; Zasloff, M.A.
Science 267, 1645-1648, 1995
A:Title: Epithelial antibiosis induced at sites of inflammation
A:Reference number: A56128; M010:55152714; PMID:7866453
A:Accession: A56128
A:Molecule type: mRNA
A:Residues: 1-64 <SCN>
A:Cross-references: GB:S76279; NID:9694238; PID:AA833327.1; PID:9594239
A:Accession: B56128
A:Molecule type: protein
A:Residues: 23-64 <SC2>
C:Keywords: antibacterial; antifungal
F:1-207/Domain: signal sequence #status predicted <Sig>
F:23-64/Product: lingual antimicrobial peptide #status experimental <MAT>
Query Match 29.2%; Score 71; DB 2; Length 64;
Best Local Similarity 44.1%; Pred. No. 0.052;
Matches 15; Conservative 1; Mismatches 16; Indels 0; Gaps 0;
QY 11 CRVRGGRCVAVLSCLPKKEQIGKCSRGRKCKCR 44
| | | | | | | | | | | | | | | | | | | | |
DB 31 CERNKGICVPIRCGSMPOIGTCLGAGVKCKCR 64
| | | | | | | | | | | | | | | | | | | | |
RESULT 4
C45495
beta-defensin-3 - bovine
N:Alternate names: peptide SNBD-3
N:Contains: beta-defensin-2
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C:Accession: C45495; B45495
R:Selsted, M.E.; Tang, Y.Q.; Morris, W.D.; McGuire, P.A.; Novotny, M.J.; Smith, K.; Hens
J.; Biol. Chem. 268, 6642-6646, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
A:Reference number: A45495; M010:93203264; PMID:8454635
A:Accession: C45495
A:Molecule type: Protein
A:Residues: 1-42 <SEL>
A:Note: sequence modified after extraction from NCBI backbone
A:Accession: B45495
A:Molecule type: protein
A:Residues: 1-42 <SE2>
A:Note: sequence extracted from NCBI backbone (NCBI:127952)
C:Keywords: antibacteria.; disulfide bond; pyroglutamic acid
F:1-42/Product: beta-defensin-3 #status experimental <MA1>
F:3-42/Product: beta-defensin-2 #status experimental <MA2>
F:2/Modified site: pyroglutonic carboxylic acid (Gln) #status experimental
F:9-38,16-31,21-39/Disulfide bonds: #status predicted
Query Match 28.4%; Score 71; DB 2; Length 42;
Best Local Similarity 40.6%; Pred. No. 0.065;
Matches 13; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
QY 11 CRVRGGRCVAVLSCLPKKEQIGKCSRGRKCKCR 42
| | | | | | | | | | | | | | | | | | | | |
DB 9 CRINRGFCVPIRCGRTQIGTCGFPPIKCCR 40
| | | | | | | | | | | | | | | | | | | | |
RESULT 5
A47438
airway epithelial antimicrobial peptide TAP precursor - bovine

N:Alternate names: antimicrobial peptide, tracheal
C:Species: Bos primigenius taurus (cattle)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: A47438; A39397
R:Blomford, G.; Jones, D.B.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 4596-4600, 1993
A:Title: Airway epithelial cells are the site of expression of a mammalian antimicro
A:Reference number: A47438; M010:93381626; PMID:6506305
A:Accession: A47438
A:Status: preliminary
A:Molecule type: cna
A:Residues: 1-64 <DIA>
A:Cross-references: GR:103373; NID:9289395; PID:AA472363.1; PID:9289395
R:Blomford, G.; Zasloff, M.; Eck, H.; Brasseur, Y.; Maioy, W.L.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 89, 3952-3956, 1992
A:Title: Tracheal antimicrobial peptide, a cysteine-rich peptide from rammalian tra
A:Reference number: A39397; M010:91234450; PMID:2023943
A:Accession: A39397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-64 <DIA>
A:Cross-references: GB:M61023; NID:92226433; PID:AA861757.1; PID:9163740
C:Genes: 1972
A:Accession: 1972
F:1-26/Domain: signal sequence #status predicted <Sig>
F:27-64/Product: airway epithelial antimicrobial peptide TAP #status predicted <MAT>
Query Match 28.4%; Score 71; DB 2; Length 64;
Best Local Similarity 41.2%; Pred. No. 0.051;
Matches 14; Conservative 3; Mismatches 17; Indels 0; Gaps 0;
QY 11 CRVRGGRCVAVLSCLPKKEQIGKCSRGRKCKCR 44
| | | | | | | | | | | | | | | | | | | | |
DB 31 CERNKGICVPIRCGSMPOIGTCLGAGVKCKCR 64
| | | | | | | | | | | | | | | | | | | | |
RESULT 6
A37903
myotoxin - eastern diamondback rattlesnake
C:Species: Crotalus adamanteus (eastern diamondback rattlesnake)
C>Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 11-Nov-1994
C:Accession: A37903
R:Saregama, Y.; Aoki, Y.; Webb, D.
Toxicol. 29, 461-469, 1991
A:Title: Amino acid sequence of a myotoxin from venom of the eastern diamondback sa
A:Reference number: A37903; M010:91320359; PMID:1866252;
A:Accession: A37903
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-45 <SAV>
A:Superfamily: Crotamine
C:Keywords: myotoxin
Query Match 27.8%; Score 69.5; DB 2; Length 45;
Best Local Similarity 38.9%; Pred. No. 0.1;
Matches 14; Conservative 4; Mismatches 15; Indels 3; Gaps 2;
QY 11 CRVRGGRCVAVLSCLPKKEQIGKCSRGRKCKCR 43
| | | | | | | | | | | | | | | | | | | | |
DB 4 CHKKGHEPPKTYTCLFPSSDFGKMDENRKKCKCK 39
| | | | | | | | | | | | | | | | | | | | |
RESULT 7
K78361
macrophage antibiotic peptide MCP-1 - rabbit
N:Alternate names: antiadrenocorticotropin, corticostatic peptide CS-3; defensin
C:Species: Cryptolagus cuniculus (domestic rabbit)
C>Date: 28-Aug-1985 #sequence_revision 23-Feb-1996 #text_change 18-Jun-1999
C:Accession: A45811; A01647; A22569; B49195
R:Ganz, T.; Rayner, J.R.; Valore, E.V.; Tumolo, A.; Talmadge, K.; Fuller, F.
J. Immunol. 143, 1358-1365, 1989
A:Title: The structure of the rabbit macrophage defensin genes and their organ-spec
A:Reference number: A45811; M010:89309825; PMID:2745593

A:Accession: A45811
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-95 <GAS>
A:Cross-references: GB:M28072; NCD:646473; PICH:AA313821; PID:646474
R:Related: M.E.: Brown, D.M.: DeLange, R.C.: Lehrer, R.I.
J. Biol. Chem. 258, 14485-14489, 1983
A:Title: Primary structures of MCP-1 and MCP-2, natural peptide antibiotics of rabbit 11
A:Reference number: A31647; MUID:8461901; PMID:6643447
A:Accession: A01647
A:Molecule type: protein
A:Residues: 63-95 <SE1>
R:Related: M.E.: Brown, D.M.: DeLange, R.J.: Harwig, S.S.L.: Lehrer, R.I.
J. Biol. Chem. 260, 4579-4584, 1985
A:Title: Primary structures of six antimicrobial peptides of rabbit peritoneal neutrophils
A:Reference number: A22569; MUID:85182561; PMID:3988726
A:Accession: A22569
A:Molecule type: protein
A:Residues: 63-95 <SE2>
A:Experimental source: peritoneal neutrophils
R:Zhu, Q.; Solomon, S.
Endocrinology 130, 1413-1423, 1992
A:Title: Isolation and mode of action of rabbit corticostatic (antiautocorticotropin)
A:Reference number: A49195; MUID:192164536; PMID:1311240
A:Accession: B49195
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 63-95 <2HU>
A:Note: sequence extracted from NCBI backbone (NCBI:P:85970)
C:Comment: This peptide is active against some fungi and gram-positive bacteria in vitro
C:Superfamily: mammalian defensin
C:Keywords: antibacterial
P:65-93,67-82,72-92/Disulfide bonds: #status predicted

Query Match 27.84; Score 69.5; DB 1; Length 95;
Best Local Similarity 48.34; Pred. No. 0.13;
Matches 14; Conservative 2; Mismatches 10; Indels 3; Gaps 1;
QY 18 CAVLSCLPKKEEQKCKSTRGR---KCCR 43
DB 67 CPRALCLPRERZAGGFR--RGR--HFLKCCR 95

RESULT 8
G45495
beta-defensin-7 - bovine
N:Alternate names: peptide BNBQ-7
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision: 22-Apr-1995 #text_change: 25-Oct-1994
R:Related: M.E.: Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.J.
J. Biol. Chem. 269, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
A:Reference number: A45495; MUID:93203264; PMID:8454635
A:Accession: G45495
A:Molecule type: protein
A:Residues: 1-40 <SE3>
A:Note: sequence modified after extraction from NCBI backbone

C:Keywords: antibacterial; disulfide bond; pyrrolidone
P:1-40/Product: beta-defensin-7 #status experimental <MA1>
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
P:38-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 27.64; Score 69; DB 2; Length 40;
Best Local Similarity 40.64; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;
QY 11 CTVRGGRCAVLSCLPKEEQKCKSTRGRKCCR 42
DB 9 CRNRGFCVPIRCQHRZQICGTCGLGPPKCCR 40

RESULT 9

145465
beta-defensin-3 - bovine
N:Alternate names: peptide BNBQ-3
N:Contains: beta-defensin-8
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision: 22-Apr-1995 #text_change: 22-Apr-1995
A:Accession: G45495; MUID:93203264; PMID:8454635
R:Related: M.E.: Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.J.
J. Biol. Chem. 269, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
A:Reference number: A45495; MUID:93203264; PMID:8454635
A:Accession: G45495
A:Molecule type: protein
A:Residues: 1-40 <SE1>
A:Note: sequence modified after extraction from NCBI backbone
A:Accession: G45495
A:Molecule type: protein
A:Residues: 1-40 <SE2>
A:Note: sequence extracted from NCBI backbone (NCBI:P:127958)
C:Keywords: pyrrolidone carboxylic acid
P:1-40/Product: beta-defensin-3 #status experimental <MA1>
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
P:38-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 27.64; Score 69; DB 2; Length 40;
Best Local Similarity 40.64; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;
QY 11 CTVRGGRCAVLSCLPKEEQKCKSTRGRKCCR 42
DB 9 CRNRGFCVPIRCQHRZQICGTCGLGPPKCCR 40

RESULT 10
D4775
beta-defensin-13 - bovine
N:Alternate names: peptide BNBQ-13
N:Contains: beta-defensin-12
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision: 18-Nov-1994 #text_change: 22-Apr-1995
A:Accession: G47753; C47753
R:Related: M.E.: Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.J.
J. Biol. Chem. 269, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
A:Reference number: A45495; MUID:93203264; PMID:8454635
A:Accession: G47753
A:Molecule type: protein
A:Residues: 1-42 <SE1>
A:Note: sequence extracted from NCBI backbone (NCBI:P:127963)
A:Accession: G47753
A:Molecule type: protein
A:Residues: 5-42 <SE2>
A:Note: sequence extracted from NCBI backbone (NCBI:P:127962)
C:Keywords: disulfide bond
P:1-42/Product: beta-defensin-13 #status experimental <MA1>
P:5-42/Product: beta-defensin-12 #status experimental <MA2>
P:9-38,16-31,21-39/Disulfide bonds: #status experimental

Query Match 27.24; Score 68; DB 2; Length 42;
Best Local Similarity 43.84; Pred. No. 0.15;
Matches 14; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY 11 CTVRGGRCAVLSCLPKEEQKCKSTRGRKCCR 42
DB 9 CCRNGGCVPIRCQHRZQICGTCGLGPPKCCR 40

RESULT 11
G3647
crocetin 3 precursor - tropical rattlesnake
C:Species: Crotales durissus terrificus (tropical rattlesnake, Cascabel)
C:Date: 14-Dec-1990 #sequence_revision: 14-Dec-1990 #text_change: 24-Jun-1993

C:Accession: C35947
R:Smith, L.A.; Schmidt, J.J.
Toxicol 28, 575-585, 1990
A:Title: Cloning and nucleotide sequences of crotaline genes.
A:Reference number: A35947; MUID:90357261; PMID:2389256
A:Accession: C35947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-65 <SMI>
C:Superfamily: crotaline

Query Match 27.0%, Score 67.5; DB 2; Length 65;
Best Local Similarity 37.8%, Pred. No. 0.25;
Matches 14; Conservative 5; Mismatches 13; Indels 5; Gaps 3;

QY 11 CRVRGGRCVAVLS--CLPKKEEQIKK--CSTRGRKCCRR 43
 ||||| || |||
DB 26 CHIKKGHCFFPKKICIPSSDFGKMDCPWR-RKCCCK 61

RESULT 12

A35947
Crotaline 1 precursor - tropical rattlesnake
C:Species: Crotalus durissus terrificus (tropical rattlesnake, cascade)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1991
C:Accession: A35947
R:Smith, L.A.; Schmidt, J.J.
Toxicol 28, 575-585, 1990
A:Title: Cloning and nucleotide sequences of crotaline genes.
A:Reference number: A35947; MUID:90357261; PMID:2389256
A:Accession: A35947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-65 <SMI>
C:Superfamily: crotaline

Query Match 27.0%, Score 67.5; DB 2; Length 65;
Best Local Similarity 37.8%, Pred. No. 0.25;
Matches 14; Conservative 5; Mismatches 13; Indels 5; Gaps 3;

QY 11 CRVRGGRCVAVLS--CLPKKEEQIKK--CSTRGRKCCRR 43
 ||||| || |||
DB 26 CHIKKGHCFFPKKICIPSSDFGKMDCPWR-RKCCCK 61

RESULT 13

CARSCH
toxic peptide C - southern Pacific rattlesnake
C:Species: Crotalus viridis helleri (southern Pacific rattlesnake)
C:Date: 31-May-1979 #sequence_revision 09-Oct-1991 #text_change 23-Aug-1996
C:Accession: A01737
R:Matada, N.; Tamiya, N.; Pattabhiraman, T.R.; Russell, F.F.
Toxicol 16, 431-441, 1978
A:Title: Some chemical properties of the venom of the rattlesnake, Crotalus viridis helleri.
A:Reference number: A01737; MUID:79015339; PMID:694946
A:Accession: A01737
A:Molecule type: protein
A:Residues: 1-43 <VAE>
C:Superfamily: crotaline
C:Keywords: myotoxin; venom
F:4-36,11-30,18-37;Disulfide bonds: #status predicted

Query Match 26.6%, Score 66.5; DB 1; Length 43;
Best Local Similarity 36.1%, Pred. No. 0.23;
Matches 13; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

QY 11 CRVRGGRC--AVLSCLPKKEEQIKKSTRGR-KCRR 43
 ||| || |||
DB 4 CHIKKGHCFFPKTVICLIPSSDFGKMDCKRWKCKCK 39

RESULT 14

CXRSMT
crotaline - tropical rattlesnake
C:Species: Crotalus durissus terrificus (tropical rattlesnake, cascade)
C:Date: 22-Jun-1991 #sequence_revision 22-Jun-1991 #text_change 23-Aug-1996
C:Accession: A01735
R:Lauro, C.J.
Heppe-Reyer's 2, Physiolo Chem 356, 213-215, 1975
A:Title: The primary structure of crotaline, a basic toxin isolated from the venom of
A:Reference number: A01735; MUID:76023761; PMID:1176086
A:Accession: A01735
A:Molecule type: protein
A:Residues: 1-42 <CAU>
C:Superfamily: crotaline
C:Keywords: myotoxin; venom
F:4-16,11-30,18-37;Disulfide bonds: #status predicted

Query Match 26.2%, Score 65.5; DB 1; Length 42;
Best Local Similarity 35.9%, Pred. No. 0.13;
Matches 14; Conservative 3; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRVRGGRCVAVLS--CLPKKEEQIKKSTRGR-KCRR 43
 ||||| || |||
DB 4 CHIKKGHCFFPKKICIPSSDFGKMDCKRWKCKCK 39

RESULT 15
C35947
crotaline 4 precursor - tropical rattlesnake (fragment)
C:Species: Crotalus durissus terrificus (tropical rattlesnake, cascade)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1991
C:Accession: A35947
R:Smith, L.A.; Schmidt, J.J.
Toxicol 28, 575-585, 1990
A:Title: Cloning and nucleotide sequences of crotaline genes.
A:Reference number: A35947; MUID:90357261; PMID:2389256
A:Accession: A35947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-61 <SMI>
C:Superfamily: crotaline

Query Match 26.2%, Score 65.5; DB 2; Length 51;
Best Local Similarity 35.1%, Pred. No. 0.35;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRVRGGRCVAVLS--CLPKKEEQIKKSTRGR-KCRR 44
 ||||| || |||
DB 12 CHIKKGHCFFPKKICIPSSDFGKMDCKRWKCKCK 48

RESULT 16

C35947
crotaline 4 precursor - tropical rattlesnake (fragment)
C:Species: Crotalus durissus terrificus (tropical rattlesnake, cascade)
C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1991
C:Accession: A35947
R:Smith, L.A.; Schmidt, J.J.
Toxicol 28, 575-585, 1990
A:Title: Cloning and nucleotide sequences of crotaline genes.
A:Reference number: A35947; MUID:90357261; PMID:2389256
A:Accession: A35947
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-61 <SMI>
C:Superfamily: crotaline

Query Match 26.2%, Score 65.5; DB 2; Length 51;
Best Local Similarity 35.1%, Pred. No. 0.35;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRVRGGRCVAVLS--CLPKKEEQIKKSTRGR-KCRR 44
 ||||| || |||
DB 12 CHIKKGHCFFPKKICIPSSDFGKMDCKRWKCKCK 48

Search completed: October 27, 2003, 14:53:29
CPU time: 1.18 sec

GeneCore version 5.1.6
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CM protein - protein search, using sw model

Run on: October 27, 2003, 14:51:57 ; Search time 11 Seconds
(without alignments)
192 382 Million cell updates/sec

Title: US-09-872-852-4
Perfect score: 250
Sequence: 1 GINTLQKYYCVRVGRCAV.....KEQYGRKSTRGRKCRRAK 45

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026735 residues 127863
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	250	100.0	67	1 D103_HUMAN	P81534 homo sapien
2	89	35.6	42	1 BD06_BOVIN	P46164 bos taurus
3	80	32.0	53	1 BD07_BOVIN	C18815 bos taurus
4	79.5	31.9	64	1 EAP_BOVIN	C62675 bos taurus
5	76	30.4	64	1 BD01_PIG	P46169 bos taurus
6	75	30.0	38	1 BD11_BOVIN	Q9W110 mus musculu
7	74.5	29.8	63	1 BD03_MOUSE	Q28980 bos taurus
8	73	29.2	64	1 LAP_BOVIN	P46160 bos taurus
9	72	28.4	40	1 BD02_BOVIN	P46167 bos taurus
10	71	28.4	55	1 BD09_BOVIN	P46162 bos taurus
11	71	28.4	57	1 BD03_BOVIN	P25068 bos taurus
12	71	28.4	64	1 TAP_BOVIN	P24330 croctalus ad
13	69.5	27.8	45	1 MYX_CRCAD	P01376 oryctolagus
14	69.5	27.8	95	1 DEFI_RABIT	P46166 bos taurus
15	69	27.5	38	1 BD08_BOVIN	P46165 bos taurus
16	69	27.6	40	1 BD07_BOVIN	C19039 ovis aries
17	68.5	27.4	64	1 BD02_SHEEP	P46120 bos taurus
18	68	27.2	38	1 BD12_BOVIN	P46121 bos taurus
19	68	27.2	42	1 BD13_BOVIN	C97346 capra hircu
20	68	27.2	64	1 BD01_CAPIH	C15253 homo sapien
21	68	27.2	64	1 BD02_HUMAN	P24331 croctalus du
22	67.5	27.0	65	1 MYX1_CROCU	P01377 croctolagus
23	67.5	27.0	65	1 MYX1_CROCU	P82020 mus musculu
24	66.5	26.6	43	1 MYX2_CRCOVH	P46163 bos taurus
25	65.5	26.2	42	1 MYX3_CRCOVH	P49831 homo sapien
26	65.5	26.2	51	1 MYX4_CRCOVH	C19038 ovis aries
27	65.5	26.2	95	1 DEFI_RABIT	P46165 tesocricellu
28	65	26.0	71	1 BD02_MOUSE	
29	64	25.6	64	1 BD05_BOVIN	
30	64	25.6	116	1 MCS_HUMAN	
31	63.5	25.4	64	1 BD01_SHEEP	
32	62.5	25.0	42	1 MYX1_CRCOV	
33	62	24.8	33	1 DEFI_MESAC	

34	61	24.4	69	1 BD11_RAT	C89117 rattus norv
35	61	24.4	69	1 AD11_HUMAN	O75076 homo sapien
36	60	24.0	773	1 AD11_MOUSE	Q91194 mus musculu
37	60	24.0	677	1 SP87_DICDI	P54643 dictyosteli
38	59	23.6	69	1 BD01_MOUSE	P56396 mus musculu
39	58.5	23.4	43	1 MYX1_CRCOV	P12028 croctalus vi
40	58.5	23.4	45	1 MYX2_CRCOV	P19861 croctalus vi
41	58.5	23.4	705	1 YMW1_YEAST	P15995 saccharomyc
42	58	23.2	34	1 DEFI_RABIT	P07468 cryctolagus
43	58	23.2	60	1 HSP1_MOUSE	P02119 mus musculu
44	58	23.2	50	1 HSP1_PAT	P10118 rattus norv
45	57.5	23.0	43	1 MYX2_CRCOV	P12029 croctalus vi

ALIGNMENTS

RESULT :
D103_HUMAN
AD D103_HUMAN STANDARD: FRT 67 AA
AD P81534 Q9NPFF6
BT 14-OCT-2001 (Rel: 40, Created)
BT 14-OCT-2001 (Rel: 40, Last sequence update)
BT 15-SEP-2003 (Rel: 42, Last annotation update)
DE Beta-defensin 3 precursor (BD-3) (BDC-3) (Beta-defensin 103) (Defensin
like protein)
GN DEFB103 CR DEFB1 CR BD3
CS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606,
[1]
[2]
RN SEQUENCE FROM N.A., SEQUENCE OF 23-47, FUNCTION, TISSUE SPECIFICITY,
INDUCTION, AND MASS SPECTROMETRY
RP TISSUE: keratinocytes, lung epithelial cells, and tracheal epithelium;
RX MEDLINE:21101950; PubMed:1108599;
RA Harder J., Bartels C., Christophers E., Schroeder J.-M.,
RT Isolation and characterization of human beta-defensin-3, a novel
human inducible peptide antibiotic.
RL J. Biol. Chem. 276:5737-5743(2001).
[3]
[4]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE:21558153; PubMed:1170237;
RA Garcia C.-R., Jaumann F., Schulz S., Krause A., Rodriguez-Cinrez J.,
Rorssmann C., Adermann K., Kluever G., Vogelmeier C., Becker D.,
Rorssmann R., Forssmann W.-G., Bais R.,
RT Identification of a novel, multifunctional beta-defensin (human
beta-defensin 3) with specific antimicrobial activity. Its
interaction with plasma membranes of xenopus oocytes and the
induction of macrophage chemotraction.
RL Cell Tissue Res. 306:257-264(2001).
[5]
RN SEQUENCE FROM N.A.
RP MEDLINE:21125233; PubMed:1223260;
RA Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guhmiller J.M.,
Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz I.,
RCray F.B., et al.
RT Discovery of new human defensins using a genomics-based approach.
RL Gene 263:211-218(2001).
[6]
RN SEQUENCE FROM N.A.
RP Submitted (FEB 2000) to the EMBL/GenBank/DBJ databases.
RA Trai V.,
RT Submitted (FEB 2000) to the EMBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A.
RA Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,
Jaspars S., Whitmore T., Fox B., Goshik C., Pixon M., Gao Z.,
Haldeman B., O'Hara P.,
RT EST and genomic database mining yield novel human and mouse
beta-defensins.
RC Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC !. FUNCTION: EXHIBITS ANTIMICROBIAL ACTIVITY AGAINST GRAM POSITIVE
BACTERIA S. AUREUS AND S. PYOGENES, GRAM-NEGATIVE BACTERIA

```
CC P. AERUGINOSA AND E. COLI AND THE YEAST CALICANS. KILLS
CC MOUTINRESISTANT S. AUREUS AND VANCOMYCIN-RESISTENT E. FAECIUM. NO
CC SIGNIFICANT HEMOLYTIC ACTIVITY WAS OBSERVED.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SKIN AND TONSILS, AND TO A
CC LESSER EXTENT IN TRACHEA, UTERUS, KIDNEY, THYMUS, ADENOID, PHARYNX
CC AND TONGUE. LOW EXPRESSION IN SALIVARY GLAND, BONE MARROW, COLON,
CC STOMACH, POLYP AND LARYNX. NO EXPRESSION IN SMALL INTESTINE.
CC -1- INDUCTION: BY INFECTION OF BACTERIA AND BY INTERFERON GAMMA.
CC -1- MASS SPECTROMETRY: MW=5154.59; K1ETHIOE-ELECTROSPRAY; RANGE=21-87.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC
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CC
CC EMBL: AJ237673; CAC03097.1;
CC EMBL: AF295370; AAG02237.1;
CC EMBL: AF217245; AAF73853.1;
CC EMBL: AB037972; BAB43572.1;
CC EMBL: AF301470; AAG22030.1;
CC DB: 1KJ6; 2C-MAR-02.
CC Genew: HGNC:15967; DBFBI03.
CC MIM: 606612.
CC GO: GO:0005767; Extracellular; NAS.
CC GO: GO:0008224; F-Gram-positive antibacterial peptide activity; TAS.
CC GO: GO:0006965; Plant-Gram-positive bacterial polypeptide in; TAS.
CC InterPro: IPR001855; Defensin_beta.
CC Pfam: PF00711; Defensin_beta.
CC Antibiotic; Signal; 3D-structure.
CC SIGNAL 1 22 BETA-DEFENSIN 3.
CC CHAIN 23 67 BY SIMILARITY.
CC DISULFID 33 62 BY SIMILARITY.
CC DISULFID 40 55 BY SIMILARITY.
CC DISULFID 45 53 BY SIMILARITY.
CC SEQUENCE 67 AA; 7697 MW; 54266DE09E54865 CRC647.
CC
CC Query Match 100.0% Score 250; DB 1; Length 67;
CC Best Local Similarity 100.0%; Pred. No. 1,7e-25;
CC Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 GIINTLQYVYGVGKRCVLSCLPKKEQIGKSTGRKCCRKK 45
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC DB 23 GIINTLQYVYGVGKRCVLSCLPKKEQIGKSTGRKCCRKK 47
CC
CC RESULT 2
CC BD06_BOVIN
CC ID BD06_BOVIN STANDARD; PRT; 42 AA.
CC P46264.
CC DT 01-NOV-1995 (Rel. 32, Created.
CC DT 01-FEB-1996 (Rel. 33, Last sequence update.
CC DT 28-FEB-2003 (Rel. 41, Last annotation update.
CC DE Beta-defensin 6 (BN6B-6) (BN6B-6).
CC GN DBF6.
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913.
CC RN 1.
CC KF SEQUENCE.
CC RC STRAIN=Hoford; TISSUE=Neutrophils;
CC RX MEDLINE=9120364; PubMed=9154835;
CC RA Seasted M.E., Tang Y.-C., Morris W.L., McGuire P.A., Novotny M.J.,
CC Smith W., Henschen A.H., Gullor J.S.
CC "Purification, primary structures, and antibacterial activities of
CC beta-defensins, a new family of antimicrobial peptides from bovine
CC neutrophils."
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CC C. Biol. Chem. 269:6641-6645 (1994).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI, MRSS
CC AND S. AUREUS AG2A.
CC -1- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC FIR: F45495; F45495.
CC HSP: P46170; DBNE.
CC InterPro: IPR016080; Defensin_beta.
CC InterPro: IPR016080; Defensin_beta.
CC Pfam: PF00711; Defensin_beta.
CC SMART: SM00048; DEFSN.
CC OS Homo sapiens.
CC KW Antibiotic; Pyroglutamate carboxylic acid.
CC FT YCD RES 1 PYROGLUTAMATE CARBOXYLIC ACID.
CC DISULFID 9 38 BY SIMILARITY.
CC DISULFID 16 31 BY SIMILARITY.
CC DISULFID 21 39 BY SIMILARITY.
CC SEQUENCE 42 AA; 4838 MW; C9EAEF82C0A897 CRC647.
CC
CC Query Match 100.0% Score 89; DB 1; Length 42;
CC Best Local Similarity 48.5%; Pred. No. 4.3e-05;
CC Matches 16; Conservative 1; Mismatches 14; Indels 0; Gaps 0.
CC
CC QY 1 CPTGSKAVLSCLPKKEQIGKSTGRKCCR 43
CC DB 9 CPTGSKAVLSCLPKKEQIGKSTGRKCCR 41
CC
CC RESULT 3
CC BD07_BOVIN
CC ID BD07_BOVIN STANDARD; PRT; 53 AA.
CC C18615.
CC DT 15-JUN-1999 (Rel. 38, Created.
CC DT 15-JUN-1999 (Rel. 38, Last sequence update.
CC DT 15-JUN-1999 (Rel. 38, Last annotation update.
CC DE Beta defensin C7 precursor (BBD(C7)) (Fragment).
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913.
CC RN 1.
CC KF SEQUENCE FROM N.A.
CC RC TISSUE=Small intestine.
CC RX MEDLINE=98147718; PubMed=9488394;
CC RA Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
CC Erdjument-Bronage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
CC Kimes M., Wang S., Bevins C.L.
CC "Enteric beta-defensin: molecular cloning and characterization of a
CC gene with inducible intestinal epithelial cell expression associated
CC with Cryptosporidium parvum infection."
CC Infect Immun 66:1043-1056 (1998).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF061951; AAC43802.1;
CC EMBL: P46170; DBNE.
CC InterPro: IPR016080; Defensin_beta.
CC InterPro: IPR016080; Defensin_beta.
CC Pfam: PF00711; Defensin_beta.
CC SMART: SM00048; DEFSN.
CC K1 Anticodon; Signal.
CC NON-TEP 1; POTENTIAL.
CC SIGNAL 1; POTENTIAL.
CC PROPEP 1;
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FT CHAIN 16 53 BETA-DEFENSIN C7
FT DISULFID 20 49 BY SIMILARITY
FT DISULFID 27 42 BY SIMILARITY
FT DISULFID 32 50 BY SIMILARITY
SQ SEQUENCE 53 AA; 5650 MW; 34659DF1A0489F4A CRC64;
Query Match 32.0%; Score 80; DB 1; Length 53;
Best Local Similarity 46.9%; Pred. No. 0.00076;
Matches 15; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 11 CRVGRGRCVLSCLPKKEIGKSTGRKCKR 42
||| | | | | | | | | | | | | | |
DB 20 CRKKGICILRCQGMPOIGTCGRPAVKCR 51
||| | | | | | | | | | | | | | |
RESULT 4
EAP BOVIN
LQ - EAP BOVIN STANDARD; PRT: 64 AA.
AC Q2276;
DT 01-NOV-1997 (Rel. 35, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DT 15-JUL-1999 (Rel. 38, Last annotation update);
DE Enteric beta-defensin precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI TaxID:9913;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE:98147718; PubMed:9488194;
RA Carver A.P., Clark D.P., Diamond G., Russell J.P.,
RA Erdjument-Bronage H., Tempst P., Chen K.S., Jones D.B., Sweeney R.W.,
RA Wines M., Wang S., Bevins C.L.;
FT "Enteric beta-defensin: molecular cloning and characterization of a
FT gene with inducible intestinal epithelial cell expression associated
FT with Cryptosporidium parvum infection."
RL Infect. Immun. 66:1045-1056(1998).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE:96014297; PubMed:8589529;
RA Gallagher D.S. Jr., Ryan A.M., Diamond G., Bevins C.L., Monack J.E.,
RA "Somatic cell mapping of beta-defensin genes to cattle syntenic group
RA U25 and fluorescence in situ localization to chromosome 27."
RL Mamm. Genome 6:554-556(1995).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).
CC -!- TISSUE SPECIFICITY: INDUCIBLY EXPRESSED IN ENTERIC EPITHELIAL
CC CELLS.
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
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SQ SEQUENCE 64 AA; 7120 MW; 7E9642A56F7A6068 CRC64;
Query Match 31.8%; Score 79.5; DB 1; Length 64;
Best Local Similarity 42.4%; Pred. No. 0.0011;
Matches 18; Conservative 2; Mismatches 19; Indels 3; Gaps 0;
QY 1 GINTQKXVCPVGRGRCVLSCLPKKEIGKSTGRKCKR 42
||| | | | | | | | | | | | | | |
DB 24 GISNPUS---CPLNKRGICVPIRCQGNLRQIGTFTPSVKCKR 62
||| | | | | | | | | | | | | | |
RESULT 5
BD01 PIG
ID - BD01 PIG STANDARD; PRT: 64 AA.
AC Q63597;
DT 15-DEC-1998 (Rel. 37, Created);
DT 15-DEC-1998 (Rel. 37, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Beta-defensin 1 precursor (BD-1) (Defensin, Beta 1).
GN DFFB1
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI TaxID:9923;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE:98196859; PubMed:95179511;
RA Zhang G., Wu H., Shi X., Gang T., Ross G., Blecha F.,
RA Zhang G., Hiratawa H., Yasue H., Wu H., Ross G.R., Troyer D.,
RA Blecha F.;
FT "Cloning and characterization of the gene for a new epithelial
FT beta-defensin. Genomic structure, chromosomal localization, and
FT evidence for its constitutive expression."
RL Biol. Chem. 274:24331-24337(1999).
CC -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC
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DE          31 CLRKKGVCMFGKCAPKMKIGTGTCTCMPQVKKCKCKRK 64

RESULT 6
BD11_BOVIN
ID   BD11_BOVIN          STANDARD;             PRT;          38 AA.
AC   P46169;
DT   01-NOV-1995 (Rel. 32, Created;
DI   01-NOV-1995 (Rel. 32, Last sequence update;
DE   16-OCT-2001 (Rel. 40, Last annotation update)
GN   Beta-defensin 11 (BNDB-11) [BNDB-11]
OS   Bos taurus (Bovine);
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovidae; Bovinae; Bos
OX   NCBI_TaxID=9913;
RN   [1];
RP   SEQUENCE.
RC   STRAIN=Hereford; TISSUE=Neutrophils;
RX   MEDLINE=93203264; PubMed=8454635;
RA   Seistad M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA   Smith A., Henschen A.H., Culler J.S.;
RT   "Purification, primary structures, and antibacterial activities of
RT   beta-defensins, a new family of antimicrobial peptides from bovine
RT   neutrophils.";
RL   J. Biol. Chem. 268:6641-6648 (1993).
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI, MRSA
CC   AND S. AUREUS 502A.
CC   -!- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
DR   PIR; E47753; E47753.
DR   HSP; P46170; IBB.
DR   InterPro: IPR001855; Defensin_beta.
DR   InterPro: IPR006080; Defensin_mammal.
DR   Pfam: PFC0711; Defensin_beta_1.
DR   SMART: SM00648; DEFSN_1.
KW   Antibiotic.
FT   DISULFID 5..34 BY SIMILARITY.
FT   DISULFID 12..27 BY SIMILARITY.
FT   DISULFID 17..35 BY SIMILARITY.
SQ   SEQUENCE 38 AA; 4163 MW; EC8ICBLC2974E3E7 CRC64;

Query Match 36.0%, Score 75, DB 1, Length 38;
Best Local Similarity 46.9%, Pred. No. 0.C024;
Matches 15; Conservative 1, Mismatches 16; Indels 0; Gaps 0;

QY 11 CRVRCGRVLSCLPRKQKCKSTRGRKCKR 42
| | | | | | | | | | | | | | | |
DB 5 CRNGGVCIPIRCIGPMPKQIGTGTGRPVKCKR 16
| | | | | | | | | | | | | | | |

RESULT 7
BD03_MOUSE
ID   BD03_MOUSE          STANDARD;             PRT;          63 AA.
AC   Q9WTLG;
DT   16-OCT-2001 (Rel. 40, Created;
DI   16-OCT-2001 (Rel. 40, Last sequence update;
DE   Beta-defensin 3 precursor (BD-3) [BD-3]
GN   DEFB3 OR BD3.
OS   Mus musculus (Mouse);
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus
OX   NCBI_TaxID=10090;
RN   [1];
RP   SEQUENCE FROM N.A.1. FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6; TISSUE=Lung;
RX   MEDLINE=9307216; PubMed=10397137;
RA   Bais R., Wang X., Weegalla R.L., Kattler S., Weiner D.J., Neils M.C.,
RA   Wilson J.M.;
RT   "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed
RT   in the epithelia of multiple organs."

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RL Infect. Immun. 67:3542-3547 (1999).
RN [2];
RP TISSUE SPECIFICITY
RC STRAIN=C57BL/6, 129/SvJ, and FVB; TISSUE=Lung;
RX MEDLINE=20178831; PubMed=10922379;
RA Jia H.P., Wewk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.P.,
RA Bevins C.L., McGray P.B. Jr.;
RT "A novel murine beta-defensin expressed in tongue, esophagus, and
RT trachea.";
RL J. Biol. Chem. 275:33114-33120 (2000).
CC -!- FUNCTION: ANTIMICROBIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIA
CC E. COLI AND P. AERUGINOSA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SALIVARY GLANDS,
CC EPIDIDYMIS, OVARY AND PANCREAS AND TO A LESSER EXTENT IN LUNG,
CC LIVER AND BRAIN. LOW OR NO EXPRESSION IN SKELETAL MUSCLE AND
CC TONGUE.
CC -!- INDUCTION: By bacterial infection.
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR   EMBL; AF093245; AAC29573.1; -
DR   EMBL; AF092929; AAC29572.1; -
DR   HSP; P46170; IBB.
DR   XGD; MG11751612; DefB3.
DR   InterPro: IPR001855; Defensin_beta.
DR   InterPro: IPR006080; Defensin_mammal.
DR   Pfam: PFC0711; Defensin_beta_1.
DR   SMART: SM00648; DEFSN_1.
KW   Antibiotic; Cleavage on pair of basic residues; Signal.
FT   SIGNAL 1..20 POTENTIAL.
FT   PROPEP 21..22 POTENTIAL.
FT   CHAIN 23..63 BETA-DEFENSIN 3.
FT   DISULFID 31..59 BY SIMILARITY.
FT   DISULFID 38..52 BY SIMILARITY.
FT   DISULFID 42..60 BY SIMILARITY.
SQ   SEQUENCE 63 AA; 7126 MW; 5D59BCAD16EA33C CRC64;

Query Match 29.8%, Score 74.57, DB 1, Length 63;
Best Local Similarity 44.1%, Pred. No. 0.C046;
Matches 15; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 11 CRVRCGRVLSCLPRKQKCKSTRGRKCKR 44
| | | | | | | | | | | | | | | |
DB 31 CLRKGRGCMNRGIGNTRGICGCVPLKCKCKRK 63
| | | | | | | | | | | | | | | |

RESULT 8
LAP_BOVIN
ID   LAP_BOVIN          STANDARD;             PRT;          64 AA.
AC   Q2R580; Q2R582;
DT   01-NOV-1997 (Rel. 35, Created;
DI   01-NOV-1997 (Rel. 35, Last sequence update;
DE   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Lingual antimicrobial peptide precursor.
GN   LAP.
OS   Bos taurus (Bovine);
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1];
RP   SEQUENCE FROM N.A.1. AND PARTIAL SEQUENCE.
RC   TISSUE=tongue epithelium;
RX   MEDLINE=95192214; PubMed=7866451;

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RA Schorwetter B.S., Stolzenberg E.D., Zasloff M.A.,
RT "Epithelial antibiotics induced at sites of inflammation."
RL Science 267:1645-1646(1995).
RM [2]
RP SEQUENCE OF 3-64 FROM N.A.
RX MEDLINE=96201562; PubMed=8613361;
RA Russell J.P., Diamond G., Tarver A.P., Scanlin T.P., Bevins C.L.,
RT "Coordinate induction of two antibiotic genes in tracheal epithelial
cells exposed to the inflammatory mediators lipopolysaccharide and
tumor necrosis factor alpha".
RI Infect. Immun. 64:1565-1568(1996).
RJ
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ZL
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ZN
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RT "Purification, primary structures, and antibacterial activities of
beta-defensins, a new family of antimicrobial peptides from bovine
neutrophils."
RL C. Biol. Chem. 269:6641-6648(1994).
RM
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DR EMBL: M26893: AAA31387.1: -
DR EMBL: M28072: AAA31389.1: -
DR PIR: A45811: WTPBM1
DR InterPro: IPR006081: Defensin_alpha
DR InterPro: IPR006080: Defensin_mamma
DR InterPro: IPR002366: Defensin_propep
DR Pfam: PF00879: Defensin_propep; 1
DR Pfam: PF00323: Defensins; 1
DR SMART: SMC0048: DEFSN; 1
DR PROSITE: PS00269: DEFENSIN; 1
KW Defensin; Antibiotic; Antiviral; Fungicide; Signal
FT SIGNAL 1 19 POTENTIAL
FT PROPEP 20 62
FT CHAIN 63 95 CORTICOSTATIN III
FT DISULFID 65 93 BY SIMILARITY
FT DISULFID 67 82 BY SIMILARITY
FT DISULFID 72 92 BY SIMILARITY
SQ SEQUENCE 95 AA: 10460 MW: 58593721BB6EF032 CRC64:
Query Match: 27.8% Score 69.5; DB 1; Length 95;
Best Local Similarity 49.3%; Pred. No. C.C.3;
Matches 14; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

QY 18 CAVUSCLPKKEQIGKQSTR---KQRR 43
Db 67 CRRALCLPRRRAGFRRGRINHPDQRR 95

RESULT 15
BD08 BOVIN
ID BDC8 BOVIN STANDARD: PRT: 38 AA.
AC P46166:
DT 01-NOV-1995 (Rel. 32, Created:
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-defensin 8 (BNDB-8) (BNDB-8).
GN DEFB8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN 1;
RP SEQUENCE.
RC STRAIN=Hereford; TISSUE=Neutrophils;
RX MEDLINE=91203264; PubMed=4454635;
RA Seibert M.E., Tang Y.-Q., Morris W.J., McGuire P.A., Novotny V.J.,
RA Smith W., Henschen A.H., Culler C.S.;
RT "Purification, primary structures, and antibacterial activities of
RT beta-defensins, a new family of antimicrobial peptides from bovine
RT neutrophils."
RT J. Biol. Chem. 269:6641-6649(1993).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI ML15
CC AND S. AUREUS 502A.
CC -1- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
DR PIR: I45495; I45495.
DR HSSP: P46170; BNB.
DR InterPro: IPR001055; Defensin_beta.
DR InterPro: IPR006080; Defensin_mamma.
DR Pfam: PF00711; Defensin_beta; 1.
DR SMART: SMC0048; DEFSN; 1.
KW Antibiotic
FT DISULFID 7 16 BY SIMILARITY
FT DISULFID 14 29 BY SIMILARITY
FT DISULFID 19 39 BY SIMILARITY
SQ SEQUENCE 38 AA: 4359 MW: C7B94D6C34127CC2 CRC64.
Query Match: 27.8% Score 62; DB 1; Length 38;
Best Local Similarity 40.4%; Pred. No. E.014;
Matches 15; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 11 CRVGGRCVLSCLFKEQIGKQSTRGKQR 42
```



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RX MEDLINE=23002622; PubMed=10531296;
RA Zhao C., Nguyen T., Liu L., Saamova O., Proden K., Lehrer G.L.
RT "Differential expression of caprine beta-defensins in digestive and
RI respiratory tissues."
RL Infect. Immun. 67:6222-6224 (1999).
DR EMBL: AJ009277; CAAC8305.1;
DR HSSP: P46170; 1BNR.
DR InterPro: IPR001855; Defensin_beta.
DR InterPro: IPR006080; Defensin_gamma.
DR Pfam: PFC0711; Defensin_beta.
DR SMART: SM00048; Defensin; 1.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 64 BETA DEFENSIN-2.
SC SEQUENCE 64 AA; 7165 MW; 867355D989FC08A CRC64;

Query Match 27.4%; Score 68.5; DB 6; Length 64;
Best Local Similarity 40.9%; Pred. No. 0.01;
Matches 18; Conservative 1; Mismatches 3; Gaps 1;

QY : GIINTLQYVYVRGRCVAVLSCUPKEEQIGKSTGRKCKRK 44
DB |||||
24 GIHRS---GVNKKVCACARCPNVQISTCHGPPVKCKRK 64

RESULT 7
Q9TF12 PRELIMINARY; PRT; 64 AA.
AC Q9TF12.
DT 01-MAY-2000 (TRENBLrel. 13; Created)
DI 01-MAY-2000 (TRENBLrel. 13; Last sequence update)
DE Beta-defensin-2 (TRENBLrel. 22; Last annotation update)
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
CX NCBI_TaxID=9598;
RN 11.
XP SEQUENCE FROM N.A.
RA Duites J.A., Jangermans J.A.M., van der Straeten T., Vervenne R.A.W.,
RA Paltansing S., Frost P.A., Hienstra P.S., Thomas A.W., Nibbeling P.H.
RT "Expression of beta-defensin-2 in chimpanzee (Pan troglodytes)."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF208855; AAF20254.1;
DR HSSP: O15263; 1FD3.
DR InterPro: IPR001855; Defensin_beta.
DR InterPro: IPR006080; Defensin_gamma.
DR Pfam: PFC0711; Defensin_beta.
DR SMART: SM00048; DEFEN; 1.
SQ SEQUENCE 64 AA; 7068 MW; B0D4542E7ACCD13 CRC64;

Query Match 27.2%; Score 68; DB 6; Length 64;
Best Local Similarity 36.4%; Pred. No. 0.035;
Matches 12; Conservative 5; Mismatches 3; Gaps 0;

QY 11 CRVKGRCVAVLSCUPKEEQIGKSTGRKCKRK 43
DB |||||
31 CLKSGAICHVFPFRRYKQIGTCGUFATKCKCK 63

RESULT 8
Q9PWF3 PRELIMINARY; PRT; 65 AA.
AC Q9PWF3.
DT 01-MAY-2000 (TRENBLrel. 13; Created)
DI 01-MAY-2000 (TRENBLrel. 13; Last sequence update)
DE Crotaline isoforn precursor.
DR CROT OR CRT-P1.
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Crotalus.
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CX NCBI_TaxID=6732;
RN 11.
XP SEQUENCE FROM N.A.
RA Radebeveron W. and:
RX MEDLINE=93114849; PubMed=10454745.
RA Radtke-Baptista G., Ogilura N., Hayashi N.A.P., Camargo M.E., Grego K.
RA Brandt A.P., Yanane T.
RT Nucleotide sequence of crotaline isoforn precursors from a single
RI South American rattlesnake (Crotalus durissus terrificus).
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF053075; AAC6624.1;
DR EMBL: AF223947; AAF3491.1;
DR EMBL: AF223946; AAF3491.1;
DR InterPro: IPR001881; Myotoxin.
DR Pfam: PFC0919; Myotoxins.
DR PRINTS: PR00283; MYOTOXIN.
DR PROSITE: PS00572; Myotoxin; 1.
DR PROSITE: PS00459; MYOTOXINS; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 65 POTENTIAL.
SC SEQUENCE 65 AA; 7519 MW; F0C9153C80CEB3 CRC64;

Query Match 24.2%; Score 66.3; DB 13; Length 65;
Best Local Similarity 38.9%; Pred. No. 0.081;
Matches 14; Conservative 3; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRVKGRCVAVLSCUPKEEQIGKSTGRKCKRK 43
DB |||||
25 QHXGCHCPFKKICLPSSDFGKDCRMWRWKCKCK 61

RESULT 9
Q8R214 PRELIMINARY; PRT; 64 AA.
AC Q8R214.
DT 01-DEC-2002 (TRENBLrel. 21; Created)
DI 01-DEC-2002 (TRENBLrel. 21; Last sequence update)
DE Putative beta defensin.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Solungnathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090.
RN 11.
XP SEQUENCE FROM N.A.
RA STRAIN=CSB1/6N, TISSUE=Testis;
RA Morrison G., Sempke G., Kilanowski F., Hill R., Dorin J.
RT Identification of murine beta defensin genes.
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC437049; CAC06892.1;
DR MED: M012178401; DefB1.
SQ SEQUENCE 64 AA; 7520 MW; DE55FD61AB98A78C CRC64;

Query Match 26.7%; Score 65; DB 11; Length 64;
Best Local Similarity 30.8%; Pred. No. 0.094;
Matches 12; Conservative 9; Mismatches 16; Indels 2; Gaps 2;

QY 7 QKYVGRVGRKCAVLSCLPKESQIGKSTGRKCKRK 45
DB |||||
26 RFLDKMNGGCEAECFTPEQKIGTCCA-NPLCKRK 62

RESULT 10
Q71749
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ID 073799 PRELIMINARY; PRT: 64 AA.
AC 073799 (TRENBLRE: 07, Created)
DT 01-AUG-1998 (TRENBLRE: 07, Last sequence update)
DT 01-AUG-1998 (TRENBLRE: 07, Last sequence update)
DT 01-DEC-2001 (TRENBLRE: 19, Last annotation update)
DE Crotamine.
GN CRO3.
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
CX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99114847; PubMed=10484745;
RA Radis-Baptista G., Ogilura N., Hayashi M.A., Canargo M.E., Grego K.F.,
RA Oliveira E.B., Yamane T.;
RA "Nucleotide sequence of crotamine isoform precursors from a single
RT South American rattlesnake (Crotalus durissus terrificus).";
RI Toxicol 37:973-984(1999).
CR EMBL: AF055988; AAC19036.1;
CR InterPro: IPR000081; Myotoxin;
CR Pfam: PF00819; Myotoxins; 1;
CR PRINTS: PR00283; MYOTOXIN;
CR PRODOM: PD005972; Myotoxin; 1;
CR PROSITE: PS00459; MYOTOXINS; 1;
SQ SEQUENCE 64 AA; 739; MW: 9876315CF34CC35 CRC64;

Query Match 25.4%; Score 63.5; DB 13; Length 64;
Best Local Similarity 36.1%; Pred. No. 0.15;
Matches 13; Conservative 4; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRVRGRCRAVLS--CLFKKEQIGKSTGR-KCGR 43
DB 25 CHKKGCHFFKKEKIC:PPSSDFGMDCKRWKCKCK 60

RESULT 11
057540 PRELIMINARY; PRT: 65 AA.
AC 057540;
DT 01-JUN-1998 (TRENBLRE: 06, Created)
DT 01-JUN-1998 (TRENBLRE: 06, Last sequence update)
DT 01-DEC-2001 (TRENBLRE: 19, Last annotation update)
DE Crotamine precursor.
GN CRO1.
OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
CX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99114847; PubMed=10484745;
RA Radis-Baptista G., Ogilura N., Hayashi M.A., Canargo M.E., Grego K.F.,
RA Oliveira E.B., Yamane T.;
RA "Nucleotide sequence of crotamine isoform precursors from a single
RT South American rattlesnake (Crotalus durissus terrificus).";
RI Toxicol 37:973-984(1999).
CR EMBL: AF044674; AAC02995.1;
CR InterPro: IPR000081; Myotoxin;
CR Pfam: PF00819; Myotoxins; 1;
CR PRINTS: PR00283; MYOTOXIN;
CR PRODOM: PD005972; Myotoxin; 1;
CR PROSITE: PS00459; MYOTOXINS; 1;
KW SIGNAL 1 22 POTENTIAL;
FT CHAIN 23 65 CROTAMINE;
SQ SEQUENCE 65 AA; 7519 MW; F840C45C5BCE33 CRC64;

Query Match 25.4%; Score 63.5; DB 13; Length 65;
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Best Local Similarity 36.1%; Pred. No. 0.16;
Matches 13; Conservative 4; Mismatches 16; Indels 3; Gaps 2;

QY 11 CRVRGRCRAVLS--CLFKKEQIGKSTGR-KCGR 43
DB 26 CHKKGCHFFKKEKIC:PPSSDFGMDCKRWKCKCK 61

RESULT 12
05R216 PRELIMINARY; PRT: 67 AA.
AC 05R216;
DT 01-JUN-2002 (TRENBLRE: 21, Created)
DT 01-JUN-2002 (TRENBLRE: 21, Last sequence update)
DT 01-MAR-2003 (TRENBLRE: 23, Last annotation update)
DE Putative beta defensin.
GN DEF9.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10100;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C58L/8N; TISSUE=Brain;
RA Morrison G., Sempia C., Kilanowski F., Hill R., Dorin J.,
RA "Identification of murine beta defensin genes."
RI Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CR EMBL: AC410647; CAC224896.1;
CR NGI: M12179187; D4189.
SQ SEQUENCE 67 AA; 7682 MW; 3591CAC0DC5E1A74 CRC64;

Query Match 25.4%; Score 63.5; DB 11; Length 67;
Best Local Similarity 29.5%; Pred. No. 0.16;
Matches 13; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

QY 2 LINTLQKYVCPVEGRCAVLSCLFKKEQIGKSTGRKCKRRK 45
DB 25 L10NSEMERCHKKGGY-YFCFSSHKYIGSGHFFKPRCKRNK 67

RESULT 13
05H4P9 PRELIMINARY; PRT: 80 AA.
AC 05H4P9;
DT 01-MAR-2001 (TRENBLRE: 15, Created)
DT 01-MAR-2001 (TRENBLRE: 15, Last sequence update)
DT 01-MAR-2003 (TRENBLRE: 23, Last annotation update)
DE EP2E.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Frohlich G., Pe C., Young L.G.;
RA "Genomic organization of the human epididymal EP2 gene and its
RT relationship to defensin genes."
RI Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CR EMBL: AY005129; AAC21882.1;
SQ SEQUENCE 80 AA; 9091 MW; CF3DE98570684C19 CRC64;

Query Match 25.2%; Score 63; DB 4; Length 80;
Best Local Similarity 34.1%; Pred. No. 0.22;
Matches 14; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

QY 1 GINTLQKYVCPVEGRCAVLSCLFKKEQIGKSTGRKCK 4;
DB 24 G1RNTI----CRMQGGICRLFFCHSGSEKKRD:CSDFWNRCC 60

RESULT 14
05Y225 PRELIMINARY; PRT: 90 AA.
ID 05Y225
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AC Q9M226;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 21, Last annotation update)
DE EP2 protein variant E
OS Pan troglodytes (Chimpanzee)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
CX NCB: TaxID=9598;
RX [1];
RF SEQUENCE FROM N.A.
RX MEDLINE=20277601; PubMed=10819450;
RA Frolich O., Po C., Murphy T., Young L.G.;
RT "Multiple promoter and splicing mRNA variants of the epididymis-
EL specific gene EP2";
RL J. Androl. 21:421-436(2000);
LR EMBL: AF263555; AAF87722.1;
SQ SEQUENCE 90 AA: 5107 MW: 982155860744019 CRC64;

Query Match 25.2% Score 63; DB 6; Length 90;
Best Local Similarity 34.1% Pred. No. 0.22;
Matches 14; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

CY 1 GIINTLQKYVCVRGGRCVLSCLPKKEQIGKSGTRGRKC 4;
D6 24 GIRNTL-----CRMCGGICRFFCHSGEKAKDCSDPWNRCC 60

RESULT 15
Q8WNZ3 PRELIMINARY; PRT; 50 AA
AC Q8WNZ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DE 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Sperm protamine P1.
OS Natalus stramineus;
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Chiroptera; Microchiroptera; Natalidae; Natalus.
CX NCB: TaxID=155340;
RX [1];
RF SEQUENCE FROM N.A.
RX STRAIN=TK15660;
RA Van Den Bussche R.A., Hofer S.R., Hansen E.M.;
RT "Characterization and phylogenetic utility of the mammalian protamine
P1 gene.";
RL Mol. Phylogenet. Evol. 21:0-0(2001).
CC -- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX BY
CC SIMILARITY.
CC -- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
DR EMBL: AF435917; AAL35571;
DR InterPro: IPR000221; Protamine_F1;
DR Pfam: PF00250; Protamine_P1;
DR PROSITE: PS00048; PROTAMINE_P1;
KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
KW Nucleosome core; Spermatogenesis;
SQ SEQUENCE 50 AA: 6678 MW: 5429995843100E CRC64;

Query Match 24.8% Score 62; DB 6; Length 50;
Best Local Similarity 32.6% Pred. No. 0.2;
Matches 14; Conservative 7; Mismatches 10; Indels 12; Gaps 1;

CY 6 LQKYVCVRGGRCVLS---CLPKKEQIGKSGTRGRKCK 45
D6 1 MARYRC -----CRGSRKRCRPRK---RCRTFRRCRGRKP 34

Search completed: October 27, 2003, 14:54:13
Job time : 37 secs
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QM protein - protein search, using sw model

Run on: October 27, 2003, 14:52:02, Search time 16 Seconds

(without alignments)
118,999 Million cell updates/sec

Title: US-09-872-852-4
Perfect score: 250
Sequence: 1 GIINTLOXYKVRGRKAV KEEGIGKSTGRKKCPRK 45
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 528717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01
Maximum Match 1001
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/prodata/2/aa/5B COMB.pep.*
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4: /cgn2_6/prodata/2/aa/6B COMB.pep.*
5: /cgn2_6/prodata/2/aa/7A COMB.pep.*
6: /cgn2_6/prodata/2/aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
Score Greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	45	4 US-09-868-659-2	Sequence 2, Appl:
2	250	100.0	67	4 US-09-868-655-4	Sequence 4, Appl:
3	250	100.0	67	4 US-09-636-399A-10	Sequence 10, Appl:
4	240	98.0	65	4 US-09-636-399A-2	Sequence 2, Appl:
5	214	85.6	45	4 US-09-636-399A-43	Sequence 43, Appl:
6	214	85.6	46	4 US-09-636-399A-41	Sequence 41, Appl:
7	214	85.6	47	4 US-09-636-399A-19	Sequence 19, Appl:
8	214	85.6	43	4 US-09-636-399A-17	Sequence 17, Appl:
9	214	85.6	49	4 US-09-636-399A-15	Sequence 15, Appl:
10	209	83.6	44	4 US-09-636-399A-44	Sequence 44, Appl:
11	209	83.6	46	4 US-09-636-399A-42	Sequence 42, Appl:
12	209	83.6	46	4 US-09-636-399A-40	Sequence 40, Appl:
13	209	83.6	47	4 US-09-636-399A-38	Sequence 38, Appl:
14	209	83.6	43	4 US-09-636-399A-36	Sequence 36, Appl:
15	206	91.2	44	4 US-09-636-399A-20	Sequence 20, Appl:
16	206	81.2	44	4 US-09-636-399A-45	Sequence 45, Appl:
17	204	81.6	43	4 US-09-636-399A-23	Sequence 23, Appl:
18	204	81.6	43	4 US-09-636-399A-47	Sequence 47, Appl:
19	203	81.2	43	4 US-09-636-399A-21	Sequence 21, Appl:
20	203	81.2	43	4 US-09-636-399A-46	Sequence 46, Appl:
21	200	90.0	42	4 US-09-636-399A-26	Sequence 26, Appl:
22	200	80.0	42	4 US-09-636-399A-49	Sequence 49, Appl:
23	199	79.6	42	4 US-09-636-399A-24	Sequence 24, Appl:
24	199	79.6	42	4 US-09-636-399A-48	Sequence 48, Appl:
25	198	79.2	42	4 US-09-636-399A-22	Sequence 22, Appl:
26	195	79.0	41	4 US-09-636-399A-27	Sequence 27, Appl:
27	195	79.0	41	4 US-09-636-399A-50	Sequence 50, Appl:

Sequence 25, Appl:
Sequence 29, Appl:
Sequence 51, Appl:
Sequence 28, Appl:
Sequence 30, Appl:
Sequence 32, Appl:
Sequence 52, Appl:
Sequence 53, Appl:
Sequence 19, Appl:
Sequence 55, Appl:
Sequence 31, Appl:
Sequence 33, Appl:
Sequence 54, Appl:
Sequence 59, Appl:
Sequence 57, Appl:
Sequence 18, Appl:
Sequence 56, Appl:
Sequence 34, Appl:

ALIGNMENTS

RESULT 1
US-09-868-659-2
Sequence 2, Application US/09868659
Patent No. 6588002
GENERAL INFORMATION:
APPLICANT: CHRISTOPHERS, ENNO
APPLICANT: HARDER, JURGEN
TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
FILE REFERENCE: SCH-1813A
CURRENT APPLICATION NUMBER: US/09/868,659
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: PCT/EP00/00776
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: DE 199 05 126.9
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: DE 199 49 436.3
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTLIT Ver. 2.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
US-09-868-659-2

Query Match: 100.0%, Score 250, DB 4, Length 45
Best Local Similarity: 100.0%, Pred NO: 1, Se: 24
Matches: 45, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY : GIINTLOXYKVRGRKAVLSCLPMEEGIGKSTGRKKCPRK 45
EQ : GIINTLOXYKVRGRKAVLSCLPMEEGIGKSTGRKKCPRK 45

RESULT 2
US-09-868-659-4
Sequence 4, Application US/09868659
Patent No. 6588002
GENERAL INFORMATION:
APPLICANT: CHRISTOPHERS, ENNO
APPLICANT: HARDER, JURGEN
TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
FILE REFERENCE: SCH-1813A
CURRENT APPLICATION NUMBER: US/09/868,659
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: PCT/EP00/00776
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: DE 199 05 126.9

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; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 199 49 436.3
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-868-659-4

Query Match          100.0%; Score 250; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 23 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 67

RESULT 3
US-09-636-399A-10
; Sequence 10, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match          100.0%; Score 250; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 23 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 67

RESULT 4
US-09-636-399A-2
; Sequence 2, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match          100.0%; Score 250; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 23 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 67

RESULT 5
US-09-636-399A-43
; Sequence 43, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT 41;
; LOCATION: 141...141;
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-43

Query Match          85.6%; Score 214; DB 4; Length 45;
Best Local Similarity 91.1%; Pred. No. 4.5e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45

RESULT 6
US-09-636-399A-41
; Sequence 41, Application US/09636399A
; Patent No. 6576755
```

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; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-2

Query Match          96.3%; Score 240; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.9e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRR 43
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 23 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRR 65

RESULT 5
US-09-636-399A-43
; Sequence 43, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT 41;
; LOCATION: 141...141;
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-43

Query Match          85.6%; Score 214; DB 4; Length 45;
Best Local Similarity 91.1%; Pred. No. 4.5e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 GIINTLQKYCYVRGGRCVAVLSCLPKKEQIGKSTRGRKCCRRKK 45

RESULT 6
US-09-636-399A-41
; Sequence 41, Application US/09636399A
; Patent No. 6576755
```

```

GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 41
LENGTH: 46
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (42)...(42)
OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met

US-09-636-399A-41

Query Match      85.6%  Score 214, DB 4, Length 46.
Best Local Similarity 91.1%  Pred. No. 4.9e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIINTLQKYICRVGRGCAVLSCLPKEEIQGKSTGRKCKRRKX 45
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DC 2 GIINTLQKYICRVGRGCAVLSCLPKEEIQGKSTGRKCKRRKX 46

RESULT 7
US-09-636-399A-39
Sequence 39, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 47
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (43)...(43)
OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met

```

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US-09-636-399A-39

Query Match      85.6%  Score 214, DB 4, Length 47.
Best Local Similarity 91.1%  Pred. No. 4.9e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIINTLQKYICRVGRGCAVLSCLPKEEIQGKSTGRKCKRRKX 45
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DC 3 GIINTLQKYICRVGRGCAVLSCLPKEEIQGKSTGRKCKRRKX 47

RESULT 8
US-09-636-399A-37
Sequence 37, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37
LENGTH: 48
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (44)...(44)
OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met

US-09-636-399A-37

Query Match      85.6%  Score 214, DB 4, Length 48.
Best Local Similarity 91.1%  Pred. No. 4.9e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIINTLQKYICRVGRGCAVLSCLPKEEIQGKSTGRKCKRRKX 45
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DC 4 GIINTLQKYICRVGRGCAVLSCLPKEEIQGKSTGRKCKRRKX 48

RESULT 9
US-09-636-399A-35
Sequence 35, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05

```

1 PRIOR APPLICATION NUMBER: 09/150,786
2 PRIOR FILING DATE: 1998-09-10
3 PRIOR APPLICATION NUMBER: 09/636,335
4 PRIOR FILING DATE: 2000-08-10
5 NUMBER OF SEQ ID NOS: 72
6 SOFTWARE: FastSeq for Windows Version 3.0
7 SEQ ID NO 35
8 LENGTH: 43
9 TYPE: PRT
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 OTHER INFORMATION: Defensin polypeptide
13 NAME/KEY: VARIANT
14 LOCATION: 145...145
15 OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-35

Query Match 55.6%, Score 214, DB 4, Length 49,
Best Local Similarity 91.1%, Pred. No. 1.9e-19,
Matches 40, Conservative 0, Mismatches 4, Indels 0, Gaps 0,

QY 1 GIINTLQYCYVRGRCVAVLSCLPKKEQICKSTGRKCKRKK 45
DB 5 GIINTLQYCYVRGRCVAVLSCLPKKEQICKSTGRKCKRKK 43

RESULT 10
US-09-636-399A-44
1 Sequence 44, Application US/09636399A
2 Patent No. 6576755
3 GENERAL INFORMATION:
4 APPLICANT: Adler, David A.
5 APPLICANT: Holloway, Nand
6 APPLICANT: Beigel-Orne, Stephanie
7 APPLICANT: Sheppard, Paul O.
8 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
9 FILE REFERENCE: 97-4402
10 CURRENT APPLICATION NUMBER: US/09/636,399A
11 PRIOR FILING DATE: 2000-08-10
12 PRIOR FILING DATE: 1997-10-05
13 PRIOR FILING DATE: 1997-10-05
14 PRIOR FILING DATE: 1997-11-05
15 PRIOR FILING DATE: 1998-09-10
16 PRIOR FILING DATE: 1998-09-10
17 PRIOR FILING DATE: 2000-08-10
18 SOFTWARE: FastSeq for Windows Version 3.0
19 SEQ ID NO 44
20 LENGTH: 44
21 TYPE: PRT
22 ORGANISM: Artificial Sequence
23 FEATURE:
24 OTHER INFORMATION: Defensin polypeptide
25 NAME/KEY: VARIANT
26 LOCATION: 141...141
27 OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-44

Query Match 81.6%, Score 209, DB 4, Length 44,
Best Local Similarity 90.9%, Pred. No. 1.9e-19,
Matches 40, Conservative 0, Mismatches 4, Indels 0, Gaps 0,

QY 1 GIINTLQYCYVRGRCVAVLSCLPKKEQICKSTGRKCKRKK 44
DB 1 GIINTLQYCYVRGRCVAVLSCLPKKEQICKSTGRKCKRKK 44

RESULT 11
US-09-636-399A-42
1 Sequence 42, Application US/09636399A

2 Patent No. 6576755
3 GENERAL INFORMATION:
4 APPLICANT: Adler, David A.
5 APPLICANT: Holloway, Nand
6 APPLICANT: Beigel-Orne, Stephanie
7 APPLICANT: Sheppard, Paul O.
8 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
9 FILE REFERENCE: 97-4402
10 CURRENT APPLICATION NUMBER: US/09/636,399A
11 PRIOR FILING DATE: 2000-08-10
12 PRIOR APPLICATION NUMBER: 60/058,335
13 PRIOR FILING DATE: 1997-10-05
14 PRIOR APPLICATION NUMBER: 60/064,294
15 PRIOR FILING DATE: 1997-11-05
16 PRIOR APPLICATION NUMBER: 09/150,786
17 PRIOR FILING DATE: 1998-09-10
18 PRIOR APPLICATION NUMBER: 09/636,335
19 PRIOR FILING DATE: 2000-08-10
20 SOFTWARE: FastSeq for Windows Version 3.0
21 SEQ ID NO 42
22 LENGTH: 45
23 TYPE: PRT
24 ORGANISM: Artificial Sequence
25 FEATURE:
26 OTHER INFORMATION: Defensin polypeptide
27 NAME/KEY: VARIANT
28 LOCATION: 143...143
29 OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-42

Query Match 81.6%, Score 209, DB 4, Length 45,
Best Local Similarity 90.9%, Pred. No. 1.9e-19,
Matches 40, Conservative 0, Mismatches 4, Indels 0, Gaps 0,

QY 1 GIINTLQYCYVRGRCVAVLSCLPKKEQICKSTGRKCKRKK 44
DB 2 GIINTLQYCYVRGRCVAVLSCLPKKEQICKSTGRKCKRKK 45

RESULT 12
US-09-636-399A-40
1 Sequence 40, Application US/09636399A
2 Patent No. 6576755
3 GENERAL INFORMATION:
4 APPLICANT: Adler, David A.
5 APPLICANT: Holloway, Nand
6 APPLICANT: Beigel-Orne, Stephanie
7 APPLICANT: Sheppard, Paul O.
8 TITLE OF INVENTION: NOVEL BETA-DEFENSINS
9 FILE REFERENCE: 97-4402
10 CURRENT APPLICATION NUMBER: US/09/636,399A
11 PRIOR FILING DATE: 2000-08-10
12 PRIOR APPLICATION NUMBER: 60/058,335
13 PRIOR FILING DATE: 1997-10-05
14 PRIOR APPLICATION NUMBER: 60/064,294
15 PRIOR FILING DATE: 1997-11-05
16 PRIOR APPLICATION NUMBER: 09/150,786
17 PRIOR FILING DATE: 1998-09-10
18 PRIOR APPLICATION NUMBER: 09/636,399
19 PRIOR FILING DATE: 2000-08-10
20 NUMBER OF SEQ ID NOS: 72
21 SOFTWARE: FastSeq for Windows Version 3.0
22 SEQ ID NO 40
23 LENGTH: 46
24 TYPE: PRT
25 ORGANISM: Artificial Sequence
26 FEATURE:
27 OTHER INFORMATION: Defensin polypeptide
28 NAME/KEY: VARIANT
29 LOCATION: 143...143

PT infections, particularly when incorporated in wound dressings, also
XX related nucleic acid
PS Claim 1: Page 17, 41pp: German.
XX This invention describes the novel active, mature human proteins (1)
CC SAP-2 and SAP-3 which have antibiotic, antibacterial, antifungal and
CC antiviral activity. (1), and their precursors, are useful for treating
CC or preventing microbial infections (caused by bacteria, fungi or
CC viruses), particularly where they (or human cells expressing them) are
CC included in wound dressings, and to produce specific antibodies (Ab) or
CC their fragments. Ab are used as diagnostic reagents, e.g. to detect a
CC deficiency of (1) or the presence of a (1) variant. This sequence
CC represents the mature human SAP-3 protein described in the record of the
CC invention.
XX
SQ Sequence 45 AA;

Query Match. 100.0%; Score 250; DB 21; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : GINTLCKYVCVRGGRCVAVLSCLPKKEQIGKSTRGRKCKRRKK 45
DB : GINTLCKYVCVRGGRCVAVLSCLPKKEQIGKSTRGRKCKRRKK 45

RESULT 2
AAOL1767
ID AAO1775? standard; peptide; 45 AA.
XX
AC AAO1776?;
XX
XX 30-AUG-2002 first entry;
XX
XX Human beta-defensin-3 derivative #2.
XX
XX Human; beta-defensin-3; HBD-3; bacterial infection; gene therapy;
XX respiratory system; cystic fibrosis; inflammation; urogenital tract;
XX antibacterial; fungicide; cytostatic; anti-inflammatory; antitumor;
XX gastrointestinal tract; septicemia; apoptosis induction; cancer.
XX
XX Homo sapiens.
XX
XX WC2002405:2-A2.
XX
XX 23-MAY-2002.
XX
XX 14-NOV-2001; 2001WO-EPI3174.
XX
XX 14-NOV-2000; 2000DE-1056365
XX 30-MAR-2001; 2001DE-1016220.
XX
XX (IEPP-) IPF PHARM GMEH.
XX
XX Fortsmann W, Kluever B, Conejo-Garcia J, Adernann K, Bais R,
XX Maegert H;
XX
XX WPI; 2002-415955/46.
XX
XX New human beta-defensin 3, useful for treating or preventing microbial
XX infection and tumors, also related nucleic acid
XX
XX Claim 2, Page 21; 36pp: German.

XX The present invention relates to human beta-defensin-3 (HBD-3) and its
XX derivatives. The peptide, its coding sequence and vectors containing the
XX coding sequence are useful in (gene) therapy and diagnosis, especially
XX for preventing or treating a wide range of microbial infections
XX (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
XX respiratory tract, especially in cases of cystic fibrosis, and
XX Helicobacter pylori, also inflammatory diseases of the gastrointestinal
XX and urogenital tracts, sepsis and yeast infections), and for inducing

CC apoptosis for treating malignant melanoma and tumors. The present
XX sequence is a derivative of human BD-3.
SQ Sequence 45 AA;
Query Match. 100.0%; Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : GINTLCKYVCVRGGRCVAVLSCLPKKEQIGKSTRGRKCKRRKK 45
DB : GINTLCKYVCVRGGRCVAVLSCLPKKEQIGKSTRGRKCKRRKK 45
RESULT 3
AAUC9709
ID AAUC9709 standard; protein; 45 AA.
XX
XX AAC09719;
XX
XX 26-MAR-2002 first entry;
XX
XX Human beta-defensin-3 (HBD-3) mature protein sequence #2.
XX
XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
XX microbial growth; microbial infection; pulmonary infection.
XX
XX Homo sapiens.
XX
XX X0270192409-A2
XX
XX C4-DFC 2001.
XX
XX C1-CLN-2001; 2001MO-US15057.
XX
XX C1-CLN-2000; 2000US-2067922.
XX
XX IOWA : UNIV IOWA RES FOUND.
XX
XX McCray PB, Tack B, Jia HP, Schutte BC;
XX
XX WPI; 2002-136302/14.
XX
XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,
XX useful for treating or preventing microbial growth or infection, or in
XX gene therapy
XX
XX Claim 2; Page 93; 110pp: English.
XX
XX The present invention relates to the isolation of a novel antimicrobial
XX peptide, human beta-defensin-3 (HBD-3). Also described is a method of
XX inhibiting growth of a microbe by introducing into a host or environment
XX the antimicrobial peptide of the invention. The peptide is useful for
XX treating or preventing microbial growth or infections, e.g. pulmonary
XX infections when administered by inhalation. The peptide can be applied
XX on a work surface or a surgical instrument for the prevention and/or
XX suppression of microbial growth. The present sequence represents
XX HBD-3 mature protein sequence #2.
XX
SQ Sequence 45 AA;
Query Match. 100.0%; Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : GINTLCKYVCVRGGRCVAVLSCLPKKEQIGKSTRGRKCKRRKK 45
DB : GINTLCKYVCVRGGRCVAVLSCLPKKEQIGKSTRGRKCKRRKK 45
RESULT 4
AAV07344
ID AAV07344 standard; protein; 45 AA.

XX Forseman K, Kluever E, Conejo-Garcia J, Agertan K, Eals R,
PI Maegert H.
XX WPI: 2002-43999/46.
XX New human beta-defensin 3: useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid
XX Claim 2: Page 23; 36pp; German.
XX The present invention relates to human beta-defensin-3 (hBD-3) and its
CC derivatives. The peptide, its coding sequence and vectors containing the
CC coding sequence are useful in (gene) therapy and diagnosis, especially
CC for preventing or treating a wide range of microbial infections
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
CC respiratory tract, especially in cases of cystic fibrosis), and
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC and urogenital tracts, sepsis and yeast infections), and for inducing
CC apoptosis for treating malignant melanoma and tumours. The present
XX sequence is a derivative of human BD-3.
SQ Sequence 67 AA:
Query Match 100.0%; Score 250; DP 23; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 GIINTLQKYCYRVRGGRCVLSCLPKKECIGKCGSTGRKCCRKK 45
DE 23 GIINTLQKYCYRVRGGRCVLSCLPKKECIGKCGSTGRKCCRKK 67
RESULT 7
AAU91016
ID AAU91016 standard: Peptide, 67 AA.
XX AAU91016;
XX 05-JUN-2002 (first entry)
DE Transplant media associated defensin peptide #17.
XX Transplant; antimicrobial peptide; pore forming agent;
KW cell surface receptor binding compound; kidney transplant;
KW cardioplegia; organ transplant; transplant rejection; defensin.
XX Homo sapiens.
XX WO200209738-A1.
XX 07-FEB-2002.
XX 27-JUL-2001; 2001WO-US23785.
XX 28-JUL-2000; 2000US-221632P.
XX 17-NOV-2000; 2000US-249602P.
XX 15-MAY-2001; 2001US-260932P.
XX MURPHY C J.
XX Murphy CJ. Reid TW. Meanalty JF.
XX WPI: 2002-26895/31.
XX Media comprising antimicrobial polypeptides or pore forming agents
PT and/or cell surface receptor binding compounds useful for the storage
PT and preservation of organs prior to transplant.
XX Claim 8: Page 29; 78pp; English
XX The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. Animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification).

CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. Animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification).
CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys stored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthier
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial defensin peptide studied in the development of the
CC transplant media
SQ Sequence 67 AA:
Query Match 100.0%; Score 250; DP 23; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 GIINTLQKYCYRVRGGRCVLSCLPKKECIGKCGSTGRKCCRKK 45
DE 23 GIINTLQKYCYRVRGGRCVLSCLPKKECIGKCGSTGRKCCRKK 67
RESULT 4
AAU91016
ID AAU91016 standard: Peptide, 67 AA.
XX AAU91016;
XX 05-JUN-2002 (first entry)
XX Transplant media associated defensin peptide #20.
XX Transplant; antimicrobial peptide; pore forming agent;
KW cell surface receptor binding compound; kidney transplant;
KW cardioplegia; organ transplant; transplant rejection; defensin.
XX Homo sapiens.
XX WO200209738-A1.
XX 07-FEB-2002.
XX 27-JUL-2001; 2001WO-US23785.
XX 28-JUL-2000; 2000US-221632P.
XX 17-NOV-2000; 2000US-249602P.
XX 15-MAY-2001; 2001US-260932P.
XX MURPHY C J.
XX Murphy CJ. Reid TW. Meanalty JF.
XX WPI: 2002-26895/31.
XX Media comprising antimicrobial polypeptides or pore forming agents
PT and/or cell surface receptor binding compounds useful for the storage
PT and preservation of organs prior to transplant.
XX Claim 8: Page 30; 78pp; English.
XX The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. Animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification).

CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys scored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthy
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial defensin peptide studied in the development of the
CC transplant media.
XX
SQ Sequence 67 AA:

Query Match: 100.0%, Score 250, DB 23, Length 67
Best Local Similarity 100.0%, Pred. No. 2e-23
Matches 45, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 45
DB 23 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 67

RESULT 9
AAU09707
ID AAU09707 standard; Protein: 67 AA.
XX
AC AAU09707:

DT 26-MAR-2002 (first entry)
XX
XX Human beta-defensin-3 (HBD-3).
DE
XX Human; antimicrobial peptide; human beta-defensin-3, HBD-3,
KW microbial growth; microbial infection; pulmonary infection.
XX
CS Homo sapiens.
XX
XX NC200192309-A2.
XX
XX 06-DEC-2001.

PF 01-JUN-2001, 200:KO:US18057.
XX
XX 01-JUN-2000, 200CUS-208792P.
XX
XX (ICMA) UNIV IOWA RES FOUND.
XX
XX McCray PB, Tack B, Jia HP, Schutte BC,
XX XPI: 2002-106302/14.
XX N-PSDB: AAS14407.

XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,
PT useful for treating or preventing microbial growth or infection, or in
PT gene therapy
XX
XX Claim 1: Page 96; 110pp; English.
XX
XX The present invention relates to the isolation of a novel antimicrobial
CC peptide, human beta-defensin 3 (HBD-3). Also described is a method of
CC inhibiting growth of a microbe by introducing into a host or environment
CC the antimicrobial peptide of the invention. The peptide is useful for
CC treating or preventing microbial growth or infections, e.g. pulmonary
CC infections when administered by inhalation. The peptide can be applied
CC on a work surface or a surgical instrument for the prevention and/or
CC suppression of microbial growth. The present sequence represents
CC HBD-3.
XX
XX
SQ Sequence 67 AA:

Query Match: 100.0%, Score 250, DB 23, Length 67
Best Local Similarity 100.0%, Pred. No. 2e-23
Matches 45, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 45
DB 23 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 67

RESULT 10
AAU09743
ID AAU09743 standard; Protein: 65 AA.
XX
AC AAU09743:

DT 01-JUL-1995 (first entry)
XX
XX Beta-defensin family member zamp1.
XX
XX Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;
KW antibody; ion flux; cytotoxic activity; mammalian cell.
XX
XX Homo sapiens.
XX
XX NC05913080-A1.
XX
XX 19-MAR-1999.

PF 10-SEP-1995, 56WD-US-0122.
XX
XX 05-NOV-1997, 97US-C964487.
XX 12-SEP-1997, 97US-C054355.
XX 12-SEP-1997, 97US-0924529.
XX 05-NOV-1997, 97US-0364294.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Adler D, Raandur N, Beigel S, Holloway JL,
XX WPI: 1999-215064/18.
XX N-PSDB: AAX29985.

XX New zamp1 polypeptide and polynucleotide, human beta-defensins
PT useful as diagnostic reagents and for treatment of microbial
PT infections, and AIDS
XX
XX Claim 1: Page 70, 79pp; English.
XX
XX This sequence represents the human zamp1 protein which is a member of the
CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical
CC composition, useful for treatment of e.g. bacterial, fungal and viral
CC infections. They are also useful pro-inflammators, for treating chronic
CC tissue damage, and for stimulating the immune response, for treatment of
CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are
CC useful for studying activity of the melanocortin family, studying ion
CC flux in cell culture, and studying cytotoxic activity against mammalian
CC cells in culture, by incubation with the cells. Zamp1 polypeptides are
CC especially useful for studying epithelial defensin induction in cell
CC culture when exposed to pathogenic stimuli
XX
XX
SQ Sequence 65 AA.

Query Match: 96.0%, Score 240, DB 20, Length 65
Best Local Similarity 100.0%, Pred. No. 3.3e-22
Matches 43, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

QY 1 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 43
DB 23 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 65

RESULT 11
AAU09708
ID AAU09708 standard; Protein: 41 AA.
XX
AC AAU09708:

QY 1 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 45
DB 23 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 67

RESULT 10
AAU09743
ID AAU09743 standard; Protein: 65 AA.
XX
AC AAU09743:

DT 01-JUL-1995 (first entry)
XX
XX Beta-defensin family member zamp1.
XX
XX Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;
KW antibody; ion flux; cytotoxic activity; mammalian cell.
XX
XX Homo sapiens.
XX
XX NC05913080-A1.
XX
XX 19-MAR-1999.

PF 10-SEP-1995, 56WD-US-0122.
XX
XX 05-NOV-1997, 97US-C964487.
XX 12-SEP-1997, 97US-C054355.
XX 12-SEP-1997, 97US-0924529.
XX 05-NOV-1997, 97US-0364294.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Adler D, Raandur N, Beigel S, Holloway JL,
XX WPI: 1999-215064/18.
XX N-PSDB: AAX29985.

XX New zamp1 polypeptide and polynucleotide, human beta-defensins
PT useful as diagnostic reagents and for treatment of microbial
PT infections, and AIDS
XX
XX Claim 1: Page 70, 79pp; English.
XX
XX This sequence represents the human zamp1 protein which is a member of the
CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical
CC composition, useful for treatment of e.g. bacterial, fungal and viral
CC infections. They are also useful pro-inflammators, for treating chronic
CC tissue damage, and for stimulating the immune response, for treatment of
CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are
CC useful for studying activity of the melanocortin family, studying ion
CC flux in cell culture, and studying cytotoxic activity against mammalian
CC cells in culture, by incubation with the cells. Zamp1 polypeptides are
CC especially useful for studying epithelial defensin induction in cell
CC culture when exposed to pathogenic stimuli
XX
XX
SQ Sequence 65 AA.

Query Match: 96.0%, Score 240, DB 20, Length 65
Best Local Similarity 100.0%, Pred. No. 3.3e-22
Matches 43, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

QY 1 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 43
DB 23 GIINTLQKYYCVRGRCGCAVLSCLPKKEQIGKCKSTRGKCKRRKX 65

RESULT 11
AAU09708
ID AAU09708 standard; Protein: 41 AA.
XX
AC AAU09708:

XX 26-MAR-2002 (first entry)
XX Human beta-defensin-3 (HBD-3) mature protein, sequence #1
DE
XX
XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
KW microbial growth; microbial infection; pulmonary infection.
XX
XX Homo sapiens.
OS
XX W0200252309-A2
PN
XX 05-DEC-2001
PD
XX 01-JUN-2001: 2001WO/US:00337.
PF
XX 01-JUN-2000: 2000US-205192P.
XX
XX TOWA : CNIV ICWA RES FOUND.
PA
XX McCray PB, Tack B, Jia HP, Schutte BC.
XX WPI: 2002:106302/14.
DR
XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,
XX useful for treating or preventing microbial growth or infection, or in
XX gene therapy .
XX
XX Claim 28; Page 97; 11pp; English.
PS
XX The present invention relates to the isolation of a novel antimicrobial
XX peptide, human beta-defensin-3 (HBD-3). Also described is a method of
XX inhibiting growth of a microbe by introducing into a host or environment
XX the antimicrobial peptide of the invention. The peptide is useful for
XX treating or preventing microbial growth or infections, e.g. pulmonary
XX infections when administered by inhalation. The peptide can be applied
XX on a work surface or a surgical instrument for the prevention and/or
XX suppression of microbial growth. The present sequence represents
XX HBD-3 mature protein sequence #1.
XX
XX Sequence 41 AA:
SQ
Query Match 92.0%; Score 230; DB 23; Length 41;
Best Local Similarity 100.0%; Pred.No. 3.5e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 5 TLQYVCRVGGRCVLSCLPKKEEQIGKSTGRKTCRRKK 45
DB : TLQYVCRVGGRCVLSCLPKKEEQIGKSTGRKTCRRKK 41

RESULT 12
AA017766
ID AA017766 standard; peptide; 40 AA.
XX
XX AA017766.
AC
XX 10-AUG-2002 (first entry)
DT
XX Human beta-defensin-3 derivative #1.
DE
XX
KW Human; beta defensin-3; HBD-3; bacterial infection; gene therapy;
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW antibacterial; fungicide; cytostatic; antiinflammatory; anticancer;
KW gastrointestinal tract; septicemia; apoptosis induction; cancer.
XX
OS Homo sapiens.
XX
XX W0200240512-A2.
PN
XX 23-MAY-2002.
PD
XX
XX 14-NOV-2001: 2001WO-EP:0174.
PF Forstmann W, Kluwey E, Conejo-Garcia C, Adermann K, Bals R;

XX 14-NOV-2000: 2000DE 1056365.
PR 30-MAR-2001: 2001DE-1016220.
XX
XX (1PFP) 1PFP PHARM GMEH.
TX
XX Forstmann W, Kluwey E, Conejo-Garcia C, Adermann K, Bals R;
FI Maegert H.
FI
XX WPI: 2002-415919/16.
XX
XX New human beta-defensin 3, useful for treating or preventing microbial
XX infection and tumors, also related nucleic acid .
XX
XX Claim 2; Page 29; 16pp; German
PS
XX The present invention relates to human beta-defensin-3 (HBD-3) and its
XX derivatives. The peptide, its coding sequence and vectors containing the
XX coding sequence are useful in gene therapy and diagnosis, especially
XX for preventing or treating a wide range of microbial infections
XX (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
XX respiratory tract, especially in cases of cystic fibrosis, and
XX Helicobacter pylori), also inflammatory diseases of the gastrointestinal
XX and urogenital tracts, sepsis and yeast infections), and for inducing
XX apoptosis for treating malignant melanoma and tumors. The present
XX sequence is a derivative of human BD-3.
XX
XX Sequence 40 AA:
SQ
Query Match 90.0%; Score 225; DB 23; Length 40;
Best Local Similarity 100.0%; Pred.No. 1.4e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 6 LQKYVCRVGGRCVLSCLPKKEEQIGKSTGRKTCRRKK 45
DB : LQKYVCRVGGRCVLSCLPKKEEQIGKSTGRKTCRRKK 40

RESULT 13
AA017765
ID AA017765 standard; peptide; 31 AA.
XX
XX AA017765;
AC
XX 10-AUG-2002 (first entry)
DT
XX Human beta-defensin-3.
DE
XX
KW Human; beta-defensin-3; HBD-3; bacterial infection; gene therapy;
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW antibacterial; fungicide; cytostatic; antiinflammatory; anticancer;
KW gastrointestinal tract; septicemia; apoptosis induction; cancer.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX Modified-site 31
XX Modified-site 31
XX (note: "may be linked to between 1 and 50 amino acids"
XX (note: "may be linked to between 1 and 50 amino acids"
XX
XX W0200240512-A2.
PN
XX 23-MAY-2002
PD
XX
XX 14-NOV-2001: 2001WO-EP:0174
PF
XX
XX 14-NOV-2000: 2000DE-1056365.
PR 30-MAR-2001: 2001DE 1016220.
XX
XX (1PFP) 1PFP PHARM GMEH.
TX
XX Forstmann W, Kluwey E, Conejo-Garcia C, Adermann K, Bals R;

PI Maegert H;
XX
D9 WPI: 2002-435959/46;
XX
XX New human beta-defensin 3, useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid .
XX
XX Claim 1; Page 23; 36pp; German.
XX
XX The present invention relates to human beta-defensin-3 (hBD-3) and its
CC derivatives. The peptide, its coding sequence and vectors containing the
CC coding sequence are useful in (gene) therapy and diagnosis, especially
CC for preventing or treating a wide range of microbial infections
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
CC respiratory tract, especially in cases of cystic fibrosis, and
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC and urogenital tracts, sepsis and yeast infections), and for inducing
CC apoptosis for treating malignant melanoma and tumors. The present
XX sequence is human BD-3.
SQ Sequence 31 AA.

Query Match 70.83; Score 177; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CRVGGRCACVLSCLPKKEQIGKCGSTRGRKCC 41
DB 1 CRVGGRCACVLSCLPKKEQIGKCGSTRGRKCC 31

RESULT 14
AAW49572
ID AAW49572 standard; peptide: 31 AA.
XX
AC AAW49572;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human beta-defensin hBD-5 peptide fragment #1.
XX
XX Defensin, human; antibacterial; anti-infectivity; contraceptive;
KW peptide therapy; infection; gastrointestinal; respiratory tract;
KW urogenital tract; skin; gland; sperm penetration; systemic disease;
KW infertility; sperm maturation; gene therapy;
KW inflammatory disease; epithelial organ; gene therapy.
XX
XX Homo sapiens
CS
XX
XX W02020204487 A2.
PN
XX
XX 17-JAN-2002.
XX
XX 11-JUL-2001; 2001NO-EP07973.
PF
XX
XX 11-JUL-2000; 2000DE-1033505.
FR
XX
XX (IPFP-1) IPF PHARM GMBH.
PA
XX
XX Forssmann W, Conejo-Garcia J, Adermann K;
P1
XX WPI: 2002-179697/23.
DR
XX
XX New defensin type peptides useful for treatment of bacterial infections
PT and for fertility control, and as a diagnostic marker of inflammatory
PT disease in epithelial organs .
XX
XX Claim 2; Page 21; 41pp; German.
PS
XX
XX This invention describes novel peptides (ii) of the defensin type which
CC have antibacterial, anti-infectivity and contraceptive activity and which
CC can be used for peptide therapy (iii) and their derivatives and
CC fragments, are used (iv) to treat bacterial infections, particularly of
CC the gastrointestinal, respiratory or urogenital tracts, or of the skin
CC and associated glands; (ii) to treat systemic diseases associated with
CC overexpression or deficiency of defensin production, particularly as
CC substitution therapy or by using (ii)-specific antibodies; (iii) to treat
CC infertility, especially where the result of disordered sperm penetration,
CC maturation, also as contraceptives; and (iv) as a diagnostic

CC the gastrointestinal, respiratory or urogenital tracts, or of the skin
CC and associated glands; (iii) to treat systemic diseases associated with
CC overexpression or deficiency of defensin production, particularly as
CC substitution therapy or by using (ii)-specific antibodies; (iii) to treat
CC infertility, especially where the result of disordered sperm penetration,
CC maturation, also as contraceptives; and (iv) as a diagnostic
CC marker of inflammatory disease in epithelial organs. Both chronic and
CC acute diseases may be treated, e.g. in intensive care. Also genes that
CC encode (i) can be used for systemic or localised gene therapy of the
CC specified diseases, in epithelial tissues or organs. (ii) have exceptional
CC biological activity and since they do not induce an immune response, they
CC are particularly well suited for long-term use. This sequence represents
XX a human defensin described in the disclosure of the invention
SQ Sequence 31 AA.

Query Match 70.83; Score 177; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 9e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CRVGGRCACVLSCLPKKEQIGKCGSTRGRKCC 41
DB 1 CRVGGRCACVLSCLPKKEQIGKCGSTRGRKCC 31

RESULT 15
AAW49576
ID AAW49576 standard; peptide: 31 AA.
XX
AC AAW49576;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human beta-defensin hBD-6 peptide fragment #2.
XX
XX Defensin, human; antibacterial; anti-infectivity; contraceptive;
KW peptide therapy; infection; gastrointestinal; respiratory tract;
KW urogenital tract; skin; gland; sperm penetration; systemic disease;
KW infertility; sperm maturation; gene therapy;
KW inflammatory disease; epithelial organ; gene therapy.
XX
XX Homo sapiens
CS
XX
XX W02020204487 A2.
PN
XX
XX 17-JAN-2002.
XX
XX 11-JUL-2001; 2001NO-EP07973.
PF
XX
XX 11-JUL-2000; 2000DE-1033505.
FR
XX
XX (IPFP-1) IPF PHARM GMBH.
PA
XX
XX Forssmann W, Conejo-Garcia J, Adermann K;
P1
XX WPI: 2002-179697/23.
DR
XX
XX New defensin type peptides useful for treatment of bacterial infections
PT and for fertility control, and as a diagnostic marker of inflammatory
PT disease in epithelial organs .
XX
XX Claim 3; Page 22; 41pp; German.
PS
XX
XX This invention describes novel peptides (ii) of the defensin type which
CC have antibacterial, anti-infectivity and contraceptive activity and which
CC can be used for peptide therapy (iii) and their derivatives and
CC fragments, are used (iv) to treat bacterial infections, particularly of
CC the gastrointestinal, respiratory or urogenital tracts, or of the skin
CC and associated glands; (ii) to treat systemic diseases associated with
CC overexpression or deficiency of defensin production, particularly as
CC substitution therapy or by using (ii)-specific antibodies; (iii) to treat
CC infertility, especially where the result of disordered sperm penetration,
CC maturation, also as contraceptives; and (iv) as a diagnostic

marker of inflammatory disease in epithelial organs. Both chronic and acute diseases may be treated, e.g. in intensive care. Also genes that encode it can be used for systemic or localised gene therapy of the specified diseases, in epithelial tissues or organs. It has exceptional biological activity and since they do not induce an immune response, they are particularly well suited for long-term use. This sequence represents a human defensin described in the disclosure of the invention

Sequence 31 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	pred. NC	9e-5
Matches	31	Conservative	0
		Mismatches	0
		Indels	0
		Gaps	0

cy 11 CRVRGRCATVSCLPKEEQIGKSTRGKCC 41
+ + + + +
db 1 CRVRGRCATVSCLPKEEQIGKSTRGKCC 31

Search completed: October 27, 2003, 14:53:06
Job time : 43 secs